

STIC Search Report Biotech-Chem Library

STIC/Database/Ina@ting

TO: Franco M Salvoza Location: REM/3B49/3C18

Art Unit: 1648

Friday, September 23, 2005

Case Serial Number: 10/654737

From: Paul Schulwitz

Location: Biotech-Chem Library

REM-1A65

Phone: 571-272-2527

Paul.schulwitz@uspto.gov

Search Notes

Examiner Salvoza,

Please review the attached search results.

If you have any questions or if you would like to refine the search query, please feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist REM-1A65 571-272-2527



STIC-Biotech/ChemLib

RUSH SEARCH APPROVED

-----Original Message-----

Searcher Phone:

Date Searcher Picked up:

Searcher Prep Time:____

Searcher:_

Online Time:_

From:

Sent:

Subject:

Importance:

To:

Cc:

Page, Thurman

Page, Thurman

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Wednesday, September 21, 2005 4:08 PM

STIC-Biotech/ChemLib; Salvoza, Franco

FW: rush sequence search request

166505

From: Sent: To: Subject:	Salvoza, Franco Wednesday, September 21, Page, Thurman rush sequence search reque	•		,	
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best regards,					
Franco Salvoza	1				
Examiner Fran AU1648 REM 3B49 x8410	co Salvoza				RECEIVED SEP 21 2015 THE CHING DIVI

Type of Search

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Structure #:___

Inventor:____

Vendors and cost where applicable
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LEXIS/NEXIS:__
SEQUENCE SYSTEM:__
WWW/Internet:__
Other (Specify):____

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OM protein

Run on:

Sequence:

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12 ; Search time 156.61 Seconds (without alignments) 568.004 Million cell updates/sec
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	Description	Aae23116 Influenza	Adol4171 Influenza	Adol4175 Influenza	Adol4178 Influenza	Abb05772 Influenza	Adol4179 Influenza	Aaw03522 Non-struc	Aae09027 Equine in	Aae09029 Equine in	Adol4177 Influenza	Adol4174 Influenza	Ado14180 Influenza	9	Ado14183 Influenza		-	Adol4172 Influenza		Aae09028 Equine in	Aawl2714 Flu NS1-H	Abu71886 Human pro	Adol4182 Influenza		Aar13175 NS1 81-RL	Aar07945 NS181RLFA
SUMMARIES	ID	AAE23116	AD014171	AD014175	AD014178	ABB05772	AD014179	AAW03522	AAE09027	AAE09029	ADO14177	AD014174	ADO14180	ADO14176	AD014183	ADO14184	AD014181	AD014172	AD014173	AAE09028	AAW12714	ABU71886	AD014182	AAR20301 .	AAR13175	AAR07945
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The present invention relates to a method for isolating viruses from various sources and for producing live attenuated influenza vaccines in a serum-free African Green monkey kidney (Vero) cell culture under conditions where alterations in the surface antigens of the virus due to adaptive selection are minimised or prevented. The method is useful for the manufacture of whole-virus vaccine, preferably attenuated live vaccine. It is useful for prophylactic or therapeutic administration against viral infection, preferably influenza virus infections. The present sequence is influenza A virus/singapore/1/57/ca (cold adapted)
NSI mutant protein. This sequence is used in the exemplification of the

invention

Aar13176 NSI_81-RL Aar13177 NSI_81-RL Aar13178 NSI_81(NA Aav72521 NSI_8703P		0		Aw35281 Porcine s Aae16491 Influenza Aar38868 Sequence Aar60195 Immunogen Aar60226 Immunogen
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ALIGNMENTS

Manufacturing live vaccine, by infecting Vero cells with virus, combining cells with serum-free cell culture medium, incubating cells in presence of protease and nuclease, harvesting virus and preparing vaccine. Attenuated influenza vaccine; prophylactic; therapeutic; infection; virucide; mutant; mutein; NS1 protein. Katinger D; Influenza A virus/singapore/1/57/ca NS1 mutant protein. (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG. Romanova J, Example 4; Page 62-63; 90pp; English. AAE23116 standard; protein; 237 AA Ferko B, 25-SEP-2001; 2001WO-EP011087. 25-SEP-2000; 2000EP-00120896 21-AUG-2002 (first entry) Egorov A, WPI; 2002-416282/44. Influenza A virus. N-PSDB; AAD37061. WO200224876-A2. 28-MAR-2002. Katinger H, Synthetic. AAE23116;

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RESULT 3
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double-stranded-KNA-activated protein kinase; phosphorylation;
translation inhibition factor; eIF2alpha; viral protein synthesis;
viral protein replication; screening method; infection.
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                                            Length 237;
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                                            Query Match 97.3%; Score 1140; DB 5; Best Local Similarity 96.1%; Pred. No. 1.2e-118; Matches 221; Conservative 7; Mismatches 2;
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10-JUN-2003; 2003US-0477453P.
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-activated protein kinase to remain in an inactive state so that it does not catalyse the phosphorylation of translation inhibition factor eff2alpha, which would otherwise inhibit viral protein synthesis and replication. The invention is useful as a (high throughput) screening method for identifying compounds having inhibitory activity against influenza virus. Compounds identified are useful in treating animals, including human infected with influenza virus. The present sequence is that of an influenza virus not structural (NS)-1 protein which is related to the method of the invention.
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                                                                                                                                                                                                                                                    94.5%; Score 1107; DB 8; Length 230; 93.5%; Pred. No. 5.9e-115;
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10-JUN-2003; 2003US-0477453P.
                                                                                                                                                                                                                                                                       Best Local Similarity 93.59
Matches 215; Conservative
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WPI; 2004-420083/39.

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This invention relates to a novel method of identifying an inhibitor of influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus noncernuctural profein-1 (NSI) or its double-stranded RNA (dsRNA) binding domain and a dsRNA that binds the protein. The invention may be useful for the production of compounds with a virus non-structural profein-1 (NSI) and double-stranded RNA. It is possible that binding of double-stranded RNA by the NSI protein in a host cell causes double-stranded-RNA cattivated profein kinase to remain in an inactive state so that it does not catalyse the phosphorylation of translation inhibition factor effzalpha, which would otherwise inhibit viral protein synthesis and replication. The invention is useful as a (high throughput) screening method for identifying compounds having inhibitory activity against influenza virus. Compounds identified are useful in treating animals, including human infected with influenza virus. The present sequence is that of an influenza virus non-structural (NS)-1 protein which is related
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Sequence 230 AA;

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ADO14178 standard; protein; 217 AA 12-AUG-2004 AD014178; ADO14178 RESULT

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Influenza A virus non-structural protein (NS)-1 #8.

influenza inhibitor; influenza virus; non-structural protein-1; NS1; double-stranded RNA; dsRNA; binding domain; virucide; double-stranded-RNA-activated protein kinase; phosphorylation; translation inhibition factor; eIF2alpha; viral protein synthesis; viral protein replication; screening method; infection.

Influenza A virus

WO2004043404-A2

27-MAY-2004.

13-NOV-2003; 2003WO-US036292.

2002US-0425661P. 2003US-0477453P. 13-NOV-2002; 10-JUN-2003; (RUTF) UNIV RUTGERS STATE NEW JERSEY.

Krug RM; Montelione GT,

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This invention relates to a novel method of identifying an inhibitor of influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus non-structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding domain and a dsRNA that binds the protein. The invention may be useful for the production of compounds with a virus non-structural protein-1 (NS1) and double-stranded RNA. It is possible that binding of double-stranded RNA, It is possible that binding of double-stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA cativated protein in a host cell causes double-stranded-RNA cativated protein fin as in an inactive state so that it does not catalyse the phosphorylation of translation inhibition factor effalpha, which would otherwise inhibit viral protein synthesis and reploation. The invention is useful as a (high throughput) screening method for identifying compounds having inhibitory activity against influenza virus, Compounds identified are useful in treating animals, including human infected with influenza virus. The present sequence is that of an influenza virus in the infected with influenza virus. The present sequence is that of an influenza virus of a virus independent in the present sequence is that of an influenza virus of the present sequence is
                                       Identifying agents useful for treating influenza virus infection comprises identifying compounds that inhibit binding between influenza virus non-structural protein-1 (NS1) and a double-stranded RNA that binds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.0%; Score 1078; DB 8;
96.3%; Pred. No. 9.5e-112;
ilve 5; Mismatches 3;
                                                                                                                                                                       Disclosure; Page 13; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 96.3
Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 217 AA;
                                                                                                                          the protein
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strain; Influenzavirus A; diagnosis; Influenza A/Udorn/72 (H3N2) Strain NS1 protein SEQ ID NO:18 Ź ABB05772 standard; protein; 237 Influenza A/Udorn/72 (H3N2) Influenza A virus; genome. (first entry) Influenzavirus A. WO200200884-A2 07-MAY-2002 ABB05772; RESULT 5 ABB05772 #X#XBX#X8X#XBX#X8XB

LIGGLEWNDNTVRVSKTLQRFAWRSSDENGRPPLTPK 217

181

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21-JUN-2001; 2001WO-US019826 23-JUN-2000; 2000US-0213650P 03-JAN-2002

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The present invention describes an isolated polynucleotide (I) having the complete sequence of the Influenza A/Udorn/72 (H3N2) strain in positive strain, antigenomic message sense. ABA93934 to ABA9394 encode the Influenza A/Udorn/72 (H3N2) strain proteins given in ABB0576 to ABB05774 from the present invention. (I) is useful for designing polymerase chain reaction (PCR) primers for use in a PCR assay to detect the presence of the corresponding virus segment in a sample or for designing and selecting peptides for use in a nerzyme linked immunosorbant assay to detect the presence of the corresponding protein produced by that segment in a sample, hence is useful in diagnosis and may be modified by mutation to generate new influenza A variant strains. ABA94945 to ABA94039 represent Influenza A/Udorn/72 (H3N2) strain sequencing primers, which are used in an example from the present invention
                                                                                                                                                 rolynucleotide encoding complete sequence of influenza A/Udorn/72 polypeptide, useful in diagnosis and for generating new influenza variant strains.
                                                                                                                                                                                                                                                   Disclosure; Page 78-79; 103pp; English.
                    8
                 (AMCY ) AMERICAN CYANAMID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208; Conservative
                                                          Galarza JM, Latham TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                    WPI; 2002-139923/18.
N-PSDB; ABA93942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 237 AA;
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Matches
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QAIMDKSIILKANFSVIFDRLETLILLRAFTEEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
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                                                                                  1 MDSNITVSSFQVDCFLWHVRKQVVDQELGDAPFLDRLRRDQKSLRGRGSTLGLNIEAATHV
                                                                                                                                        1 MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETAIRA
                               Gaps
                                                                                                                                                                                                                                                 LIGGLEWNNNTVRVSKTLQRFAWRSSNENGRPPLTPKOKRKMARTIRSEV 230
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0
91.7%; Score 1075; DB 5; Length 237; 90.4%; Pred. No. 2.3e-111; tive 10; Mismatches 12; Indels C
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ADO14179 standard; protein; 227 AA 12-AUG-2004 ADO14179; AD014179 RESULT XBX5X8X5555X6X8X6X

Influenza A virus non-structural protein (NS)-1 #9. (first entry)

influenza inhibitor; influenza virus; non-structural protein-1; NS1; double-stranded RNA; dsRNA; binding domain; virucide; double-stranded-RNA-activated protein kinase; phosphorylation; translation inhibition factor; eff2alpha; viral protein synthesis; viral protein replication; screening method; infection.

MO2004043404-A2

27-MAY-2004

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This invention relates to a novel method of identifying an inhibitor of influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus nonstructural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding contain and a dsRNA that binds the protein. The invention may be useful contained to production of compounds with a virucide activity acting as inhibitors of binding between influenza virus non-structural protein-1 (NS1) and double-stranded RNA. It is possible that binding of double-stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA cativated protein kinase to remain in an inactive state so that it does not catalyse the phosphorylation of translation inhibition factor catalyse the phosphorylation of translation inhibition factor creplication. The invention is useful as a (high throughput) screening centrol dentifying compounds having inhibitory activity against continuing human infected with influenza virus. The present sequence is including human infected with influenza virus. The present sequence is that of an influenza virus non-structural (NS)-1 protein which is related
                                                                                                                                                                                                         Identifying agents useful for treating influenza virus infection comprises identifying compounds that inhibit binding between influenza virus non-structural protein-1 (NSI) and a double-stranded RNA that binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 IVERILKEESDEALKONTWASAPASRYLTDMTIEEMSRDWFMLMPKQKVAGPLCIRMDQAI 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 GLEWNNTVRVSKTLORFAWRSSNENGRPPLTPKOKRKMARTIRSEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 90.2%; Score 1057; DB 8; Best Local Similarity 90.7%; Pred. No. 2.3e-109; Matches 206; Conservative 11; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Non-structural protein NS1 of influenza A virus.
                                                                                          (RUTF ) UNIV RUTGERS STATE NEW JERSEY
                                                                                                                                                                                                                                                                                                            Disclosure; Page 13; 92pp; English.
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                                  13-NOV-2002; 2002US-0425661P.
10-JUN-2003; 2003US-0477453P.
13-NOV-2003; 2003WO-US036292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                 Montelione GT, Krug RM;
                                                                                                                                                                      WPI; 2004-420083/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 227 AA;
                                                                                                                                                                                                                                                                       the protein.
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The patent discloses cold-adapted equine influenza viruses and reassortant influenza A viruses comprising atleast one genome segment of such an equine influenza virus, wherein the equine influenza virus genome segment confers atleast one identifying phenotype of the cold-adapted equine influenza virus, such as cold adaptation, temperature sensitivity, dominant interference or attenuation. The viruses are useful for protecting animals from diseases caused by influenza viruses. They are also used as vaccines. The present sequence is an equine influenza (ei) virus H3N8 Peiwtl (wild type) NS230 protein which is encoded by neiwtlNS891 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated equine influenza virus (wild-type and cold-adapted) proteins and viruses containing nucleic acid molecules encoding the proteins, which are useful for protecting animals from influenza virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GKQIVERILKEBSDBALKMTMASAPASRYLTDMTIEEMSRDWFMLMPKQKVAGPLCIRMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GKQIVEQILEEESDEALKMTIASVPASRYLTDMTLDEMSRDWFMLMPKQKVTGSLCIRMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETAIRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  temperature sensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 LIGGLEWINNTVRVSKTLORFAWRSSNENGRPPLTPKOKRKMARTIRSEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.8%; Score 1052; DB 4;
87.8%; Pred. No. 8.4e-109;
iive 16; Mismatches 12;
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vaccine; neicalNS888 DNA; PeicalNS230 protein.
                                                                                                                                                                                                                                                           Claim 5; Page 72-73; 172pp; English.
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16-FEB-2000; 2000US-00506286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-FEB-2001; 2001WO-US005048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 202; Conservative
                                                                         Youngner JS
                                  (UYPI-) UNIV PITTSBURGH
                                                                                                         2001-522584/57
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Best Local Similarity
                                                                                                                              N-PSDB; AAD15678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200160849-A2
                                                                       Dowling PW,
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                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents non-structural protein NS1 of influenza virus A/equine 2/Suffolk 89. The NS1 protein is useful for diagnosis of equine influenza A infections by detection of anti-NS1 antibodies. The NS1 coding sequence was isolated using the primer sequences given in AAT37436-40. (Updated on 16-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                Recombinant equine influenza virus NS1 protein - useful for diagnosis of equine influenza A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIGGLEMNNTVRVSKTLQRFAWRSSNENGRPPLTPKQKRKMARTIRSEV 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Equine influenza virus H3N8 PeiwtlNS230 protein.
                 Influenza virus; A/equine 1/Suffolk 89.
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                                                                                                                                                                 95GB-00002489.
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                                                                                                                                                                                                    (ANIM-) ANIMAL HEALTH TRUST
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Matches 203; Conservative
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                                                                                                                                                                                                                                          Binns M, Birch-Machin I;
                                                                                                                                                                                                                                                                              WPI; 1996-364394/37
                                                                                                                                                                                                                                                                                                  N-PSDB; AAT37435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 230 AA;
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                                                                                                                                                                 09-PEB-1995;
                                                                                                                            31-JAN-1996;
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                                                                                          14-AUG-1996
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(UYPI-) UNIV PITTSBURGH

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reassortant influenza A viruses comprising atleast one genome segment of such an equine influenza virus, wherein the equine influenza virus genome segment confers atleast one identifying phenotype of the cold-adapted equine influenza virus, such as cold adaptation, temperature sensitivity, dominant interference or attenuation. The viruses are useful for also used as vaccines. The present sequence is equine influenza viruses. They are virus H3N8 Peical (cold adapted) NS230 protein which is encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GKQIVERILKEESDEALKWIWASAPASRYLIDWIIEEMSRDWFWLMPKQKVAGPLCIRWD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAIMDKSIILKANFSVIFDRLETLILLRAFTEEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated equine influenza virus (wild-type and cold-adapted) proteins and viruses containing nucleic acid molecules encoding the proteins, which are useful for protecting animals from influenza virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDSNIVSSFQVDCFLWHVRKRFADQELGDAPFLDRLRRDQKSLKGRGSTLGLDIETATRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETAIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           influenza inhibitor; influenza virus; non-structural protein-1; NS1; double-stranded RNA; dsRNA; binding domain; virucide; double-stranded-RNA-activated protein kinase; phosphorylation; translation inhibition factor; eff2alpha; viral protein synthesis; viral protein replication; screening method; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIGGLEWINNTVRVSKTLQRFAWRSSNENGRPPLTPKOKRKMARTIRSEV 230
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                                                                                                                                                                                                                                The patent discloses cold-adapted equine influenza viruses and
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Influenza A virus non-structural protein (NS)-1 #7
                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.8%; Score 1052; DB 4;
87.8%; Pred. No. 8.4e-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADO14177 standard; protein; 227 AA.
                                                                                                                                                                                               Claim 5; Page 77; 172pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                            Youngner JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 202; Conservative
                                                             WPI: 2001-522584/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Influenza A virus
                                                                              N-PSDB; AAD15681
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 230 AA;
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                                                                                                                                                                                                                                                                                                                                                                                  neicalNS888 DNA
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                            Dowling PW,
                                                                                                                                                                 infections.
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This invention relates to a novel method of identifying an inhibitor of influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus non-structural protein-1 (NSI) or its double-stranded RNA (dsRNA) binding domain and a dsRNA that binds the protein. The invention may be useful for the production of compounds with a virucide activity acting as inhibitors of binding between influenza virus non-structural protein-1 (NSI) and double-stranded RNA. It is possible that binding of double-stranded RNA by the NSI protein in a host cell causes double-stranded-RNA cativated protein kinase to remain in an inactive state so that it does not catalyse the phosphorylation of translation inhibition factor catalyse the phosphorylation of translation inhibition factor catzlapha, which would otherwise inhibit viral protein synthesis and catched for identifying compounds having inhibitory activity against influenza virus. Compounds identified are useful in treating animals, including human infected with influenza virus. The present sequence is that of an influenza virus non-structural (NS)-1 protein which is related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
                                                                                                                                                   Identifying agents useful for treating influenza virus infection comprises identifying compounds that inhibit binding between influenza virus non-structural protein-1 (NSI) and a double-stranded RNA that binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 NIVSSPQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETAIRAGKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 IVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWFWLMPKQKVAGPLCIRMDQAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IVERILVEESDEALKATIVSMPASRYLTDATLEEMSRDWFWLMFKQKVAGSLCIRMDQAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      influenza inhibitor; influenza virus; non-structural protein-1; NS1; double-stranded RNA; dsRNA; binding domain; virucide; double-stranded-RNA-activated protein kinase; phosphorylation; translation inhibition factor; eIF2alpha; viral protein synthesis; viral protein replication; screening method; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 GLEWNNTTVRVSKTLORFAWRSSNENGRPPLTPKOKRKMARTIRSEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Influenza A virus non-structural protein (NS)-1 #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1050; DB 8;
Pred. No. 1.4e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Mismatches
                                   (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
                                                                                                                                                                                                                                                        Disclosure; Page 13; 92pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.6%;
10-JUN-2003; 2003US-0477453P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 89.6
Best Local Similarity 91.2
Matches 207; Conservative
                                                                                                                  WPI; 2004-420083/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 227 AA;
                                                                            Montelione GT,
                                                                                                                                                                                                                     the protein.
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influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus nonservatural protein-1 (NS1) or its double-stranded RNA (BRNA) binding domain and a dsRNA that binds the protein. The invention may be useful for the production of compounds with a virucide activity acting as inhibitors of binding between influenza virus non-structural protein-1 or that binding of double-stranded RNA. It is possible that binding of double-stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA activated protein kinase to remain in an inactive state so that it does not catalyse the phosphorylation of translation inhibition factor ergalphe, which would otherwise inhibit viral protein synthesis and replication. The invention is useful as a (high throughput) screening method for identifying compounds having inhibitory activity against including human infected with influenza virus. The present sequence is that of an influenza virus non-structural (NS)-1 protein which is related to the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                          Identifying agents useful for treating influenza virus infection comprises identifying compounds that inhibit binding between influenza virus non-structural protein-1 (NS1) and a double-stranded RNA that binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel method of identifying an inhibitor
                                                                                                                                                                                                                                                    (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 12; 92pp; English
                                                                                                                                      13-NOV-2003; 2003WO-US036292.
                                                                                                                                                                              13-NOV-2002; 2002US-042566IP.
10-JUN-2003; 2003US-0477453P.
                                                                                                                                                                                                                                                                                                 Montelione GT, Krug RM;
                                                                                                                                                                                                                                                                                                                                               WPI; 2004-420083/39
Influenza A virus.
                                             WO2004043404-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               the protein.
                                                                                        27-MAY-2004
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Sequence 230 AA;

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120
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                                                                              1 MDSNTVSSFQVDCFLWHVRKRFADQEMGDAPFLDRLRRDQKSLGGRGSTLGLDIETATRA
                                                              1 MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETAIRA
                                                                                                                           GKQIVERILKEESDEALKWTWASAPASRYLTDMTIEEMSRDWFMLMPKQKVAGPLCIRMD
                                 0; Gaps
                                                                                                                                                                                                                                                   LIGGLEWINNTVRVSKTLORPAWESSNENGRPPLTPROKRRARTIRSEV 230
89.3%; Score 1047; DB 8; Length 230; 88.7%; Pred. No. 3e-108; ive 13; Mismatches 13; Indels (
                                 Matches 204; Conservative
                   Similarity
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    Query Match
Best Local S
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Indels

13;

8; Mismatches

Best Local Similarity 90.7 Matches 206, Conservative

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Query Match

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63 9

4 NTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETAIRAGKQ NTVSSFQVDCFLWHVRKRFADLELGDAPFLDRLCRDQKSLRGRSSTLGLDIBTATRAGKQ

89.2%; Score 1046; DB 8; Length 227; 90.7%; Pred. No. 3.9e-108;

123 120 183 180

64 IVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWFMLMPKQKVAGPLCIRMDQAI

MDKSIILKANFSVIFDRLETLILLRAFTEEGAIVGEISPLPSLPGHTNEDIKNAIGVLIG

124 121 184 181

GLEWNNITVRVSKTLORFAWRSSNENGRPPLTPKOKRKMARTIRSEV 230

GLEWNDNIVRVSETLQRFAWRSSNEGGRPPLPPKQKRKMARTIESEV

227

ADO14180 standard; protein; 227 AA (first entry) 12-AUG-2004 ADO14180; 181 AD014180 SXXXE

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influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus nonstructural protein-1 (NS1) or its double-stranded RNA) binding compounds with a virucide activity acting as inhibitors of binding between influenza virus non-structural protein-1 (NS1) and double-stranded RNA. It is possible that binding of double-stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA activated protein kinase to remain in an inactive state so that it does not catalyse the phosphorylation of translation inhibition factor elf2alpha, which would otherwise inhibit viral protein synthesis and reploation. The invention is useful as a (high throughput) screening method for identifying compounds having inhibitory activity against including human infected with influenza virus. The present sequence is including human infected with influenza virus the present sequence is that of an influenza virus on-structural (NS)-1 protein which is related.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying agents useful for treating influenza virus infection comprises identifying compounds that inhibit binding between influenza virus non-structural protein-1 (NSI) and a double-stranded RNA that binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a novel method of identifying an inhibitor of
                                                          influenza inhibitor; influenza virus; non-structural protein-1; NS1; double-stranded RNA; dsRNA; binding domain; virucide; double-stranded-RNA-activated protein kinase; phosphorylation; translation inhibition factor; eIFZalpha; viral protein synthesis; viral protein replication; screening method; infection.
                  Influenza A virus non-structural protein (NS)-1 #10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 13-14; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RUTF ) UNIV RUTGERS STATE NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                 13-NOV-2002; 2002US-042566IP.
10-JUN-2003; 2003US-0477453P.
                                                                                                                                                                                                                                                                                                                                      13-NOV-2003; 2003WO-US036292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Montelione GT, Krug RM;
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                                                                                                                                                                                                Influenza A virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 227 AA;
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influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus nonstructural protein-1 [NSI) or its double-stranded RNA (dsRNA) binding domain and a dsRNA that binds the protein. The invention may be useful for the production of compounds with a virucide activity acting as inhibitors of binding between influenza virus non-structural protein-1 (NSI) and double-stranded RNA. It is possible that binding of double-stranded RNA by the NSI protein in a host cell causes double-stranded-RNA cativated protein kinase to remain in an inactive state so that it does not catalyse the phosphorylation of translation inhibition factor elf2alpha, which would otherwise inhibit viral protein synthesis and method for identifying compounds having inhibitory activity against influenza virus. Compounds identified are useful in treating animals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying agents useful for treating influenza virus infection comprises identifying compounds that inhibit binding between influenza virus non-structural protein-1 (NS1) and a double-stranded RNA that binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               including human infected with influenza virus. The present sequence is that of an influenza virus non-structural (NS)-1 protein which is related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a novel method of identifying an inhibitor of
                                                                                                                                                                                           inhibitor; influenza virus; non-structural protein-1; NS1;
                                                                                                                                                                                                             double-stranded RNA; dsRNA; binding domain; virucide;
double-stranded-KNA-activated protein kinase; phosphorylation;
translation inhibition factor; elF2alpha; viral protein synthesis;
viral protein replication; screening method; infection.
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                                                                                                                                                      Influenza A virus non-structural protein (NS)-1 #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
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                                      ADO14176 standard; protein; 230 AA
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2003US-0477453P.
                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Krug
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                                                                                                                                                                                                                                                                                                              Influenza A virus
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                                                                                                                                                                                                                                                                                                                                                     WO2004043404-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Montelione GT,
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10-JUN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the protein.
                                                                                                                 12-AUG-2004
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                                                                           AD014176;
RESULT 13
                    AD014176
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This invention relates to a novel method of identifying an inhibitor of influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus non-structural protein-1 (NSI) or its double-stranded RNA (dsRNA) binding domain and a dsRNA that binds the protein. The invention may be useful correction of compounds with a virucide activity acting as inhibitors of binding between influenza virus non-structural protein-1 (NSI) and double-stranded RNA. It is possible that binding of double-stranded RNA by the NSI protein in a host cell causes double-stranded-RNA cativated protein in a host cell causes double-stranded-RNA catalyse the phosphorylation of translation inhibition factor of Erzalpha, which would otherwise inhibit viral protein synthesis and replication. The invention is useful as a (high throughput) screening method for identifying compounds having inhibitory activity against including human infected with influenza virus. The present sequence is chat of an influenza virus non-structural (NS)-1 protein which is related to the method of the invention.
                                                                           180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying agents useful for treating influenza virus infection comprises identifying compounds that inhibit binding between influenza virus non-structural protein-1 (NS1) and a double-stranded RNA that binds
                                                          GKQIVERILBEESNEALKMTIASVPASRYLTDMTLEEMSRDWFMLMPKQKVAGSLCIRMD
                                      QAIMDKSIILKANFSVIFDRLETLILLRAFTEEGAIVGEISPLPSLPGHTNEDIKNAIGV
                                                                                                                                                                                                                                                                                                                                                                                                          influenza inhibitor; influenza virus; non-structural protein-1; NS1; double-stranded RNA; dsRNA; binding domain; virucide; double-stranded-RNA-activated protein kinase; phosphorylation; translation inhibition factor; eIF2alpha; viral protein synthesis; viral protein replication; screening method; infection.
                                                                                                                 230
                                                                                                                                      181 LIGGLEWINNTVRVSKTLQRFAWRSSNENGRPPLTPKQKRKMARTIRSEV
                                                                                                                                                                                                                                                                                                                                                                       Influenza A virus non-structural protein (NS)-1 #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Influenza A virus; A/Turkey/Oregon/71(H7).
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                                                                                                                                                                                                                                                       ADO14183 standard; protein; 230 AA
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10-JUN-2003; 2003US-0477453P
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DB 8; Length 230;

87.1%; Score 1021;

Query Match

61 GKQIVERILKEESDEALKWTMASAPASRYLTDWTIEEMSRDWFWLMPKOKVAGPLCIRMD 120

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1 MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETAIRA

Best Local Similarity 88.3 Matches 203; Conservative

Query Match

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                                                                                              GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWFMLMPKQKVAGPLCIRMD
                                          1 MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETAIRA
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Pred. No. 2.5e-105;
; Mismatches 17; Indels
 11 Similarity 85.7%; Pre 197; Conservative 16;
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AD014184 RESULT

ADO14184 standard; protein; 202 AA

ADO14184;

(first entry) 12-AUG-2004 Influenza A virus non-structural protein (NS)-1 #14.

influenza inhibitor; influenza virus; non-structural protein-1; NS1; double-stranded RNA; dsRNA; binding domain; virucide; double-stranded-ENN-activated protein kinase; phosphorylation; translation inhibition factor; eIF2alpha; viral protein synthesis; viral protein replication; screening method; infection. CCCCCCCCCCCCX2X44444X3X1X3X3X4X6X6X6X6X6X6X6X4X4X

Influenza A virus; STRAIN A/FORT MONMOUTH/1/47

WO2004043404-A2

27-MAY-2004

13-NOV-2003; 2003WO-US036292.

13-NOV-2002; 2002US-0425661P. 10-JUN-2003; 2003US-0477453P.

(RUTF) UNIV RUTGERS STATE NEW JERSEY.

Montelione GT, Krug RM;

WPI; 2004-420083/39

Identifying agents useful for treating influenza virus infection comprises identifying compounds that inhibit binding between influenza virus non-structural protein-1 (NS1) and a double-stranded RNA that binds the protein

Disclosure, Page 14; 92pp; English.

This invention relates to a novel method of identifying an inhibitor of influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus nonstructural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding domain and a dsRNA that binds the protein. The invention may be useful for the production of compounds with a virus non-structural protein-1 inhibitors of binding between influenza virus non-structural protein-1 (NS1) and double-stranded RNA. It is possible that binding of double-stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA-activated protein kinase to remain in an inactive state so that it does not catalyse the phosphorylation of translation inhibition factor elepatable, which would otherwise inhibit viral protein synthesis and replication. The invention is useful as a (high throughput) screening

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method for identifying compounds having inhibitory activity against influenza virus. Compounds identified are useful in treating animals, including human infected with influenza virus. The present sequence is that of an influenza virus non-structural (NS)-1 protein which is related to the method of the invention.
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us-10-654-737-5.rpr

Sequence:

Title:

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C;Species: influenza A virus
C;Species: influenza A virus
C;Date: 14-Nov-1983 #sequence revision 14-Nov-1983 #text_change 16-Jul-1999
C;Accession: A92991; A04090; B92982
C;Accession: A92991; A04090; B92982
J; Virol. 45, 547-554, 1983
A;Title: Sequential mutations in the NS genes of influenza virus field strains.
A;Reference number: A92991; MUID:83164298; PMID:6834468
A;Accession: A92991
A;Molecule type: genomic RNA
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1 MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETAIRA

Ouery Match 97.3%; Score 1140; DB 1; Length 237; Best Local Similarity 96.5%; Pred. No. 4.6e-91; Matches 222; Conservative 6; Mismatches 2; Indels

A,Cross-references: GB: K00576; NID:g324813; PIDN:AAA43525.1; PID:g324815 C;Genetics: segment 8 A;Map position: segment 8 C;Superfamily: influenza virus nonstructural protein NS1 C;Keywords: alternative splicing

A;Residues: 1-237 <KRY>

Gaps

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nonstructural protein NSI - influenza A virus (strain A/PR/8/34)
C;Species: influenza A virus
RESULT 4
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LIGGLEWNNTVRVSKTLQRFAWRSSNENGRPPLTPKQKRKMARTIRSEV 230

181

1 MDPNIVSSFQVDCFLWHVRKQVADQELGDAPFLDRLRRDQKSLKGRGSTLGLDIETATCV 60

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1 MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETAIRA

Query Match 96.2%; Score 1128; DB 1; Length 237; Best Local Similarity 95.2%; Pred. No. 5e-90; Matches 219; Conservative 7; Mismatches 4; Indels

A;Map position: segment 8 C;Superfamily: influenza virus nonstructural protein NS1 C;Keywords: alternative splicing; nonstructural protein

Gaps

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C;Species: influenza A virus
C;Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 19-May-2000
C;Accession: S09648
R;Beklemishev, A.B.; Blinov, V.M.; Vassilenko, S.K.; Golovin, S.Y.; Karginov, V.A.; Mamat Bioorg. Khim. 11, 641-645, 1985
A;Title: Synthesis, cloning and sequencing of a full-length DNA copy of the fragment 8 of A;Reference number: S09648; MUID:85307107; PMID:4038350
            C;Accession: A04089
R;Baez, M.; Taussig, R.; Zazra, J.J.; Young, J.F.; Palese, P.; Reisfeld, A.; Skalka, A.M.
Nucleic Acids Res. 8, 5845-5858, 1980
A;Title: Complete nucleotide sequence of the influenza A/PR/8/34 virus NS gene and compan A;Reference number: A93714; MUID:81124304; PMID:7465426
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Date: 30-Apr-1981 #sequence_revision 30-Apr-1981 #text_change 30-Sep-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GKQIVERILKEESDEALKWIMASAPASRYLIDMIIBEMSRDWFMLMPKQKVAGPLCIRMD
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C,Superfamily: influenza virus nonstructural protein NS1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 94.8%; Score 1111; DB 1; Length 230; Best Local Similarity 93.9%; Pred. No. 1.4e-88; Matches 216; Conservative 9; Mismatches 5; Indels
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C;Superfamily: influenza virus nonstructural protein NS1
C;Keywords: alternative splicing
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A;Status: preliminary; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                             A; Molecule type: genomic RNA A; Residues: 1-230 < BAE>
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A;Reference number: A34215; MUID:89345097; PMID:2762132
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nonstructural protein NS1 - influenza A virus (strain A/Chile/1/83 [HIN1]) C;Species: influenza A virus C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 07-Jun-1996 C;Accession: A34215; S04836

RESULT 3

Rischreier, E.; Roeske, H.; Michel, S. Nucleic Acids Res. 17, 5381, 1989 A; Title: Nucleotide sequence of the NS

A; Status: translation not shown

A, Accession: A34215

A; Molecule type: mRNA A; Residues: 1-237 <SCH>

A; Cross-references: EMBL:X15282

181 LIGGLEWINNTVRVSKTLORFAWRSSNENGRPPLIPKOKRKMARTIRSEV 230

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C;Accession: G31831
R;Cox, N.J.; Kitame, F.; Kendal, A.P.; Maassab, H.F.; Naeve, C.
Virology 167, 554-567, 1988
A;Title: Identification of sequence changes in the cold-adapted, live attenuated influen:
A;Reference number: A31831; MUID:89073759; PMID:2974219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: GB:M23968; GB:J04349; GB:M23969; NID:G324860; PIDN:AAA43553.1; PID:G
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C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
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C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
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                       1 MDPNTVSSFQVDCFLWHVRKQVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETATRV
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91.7%; Score 1075; DB 1; Length 230;
Best Local Similarity 91.3%; Pred. No. 1.8e-85;
Matches 210; Conservative 9; Mismatches 11; Indels (
                                                                                                                                              181 LIGGLEWNDNTVRVSETLQRFAWRSSNEGGRPPLPPKQKRKMARTIESEV
                                                                                                                 181 LIGGLEWNNNTVRVSKTLQRFAWRSSNENGRPPLTPKQKRKMARTIRSEV
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Ritreanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R. Virology 171, 1-9, 1989
A;Title: The Ballele of the NS gene of avian influenza v
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C;Superfamily: influenza virus nonstructural protein NS1
C;Reywords: alternative splicing; nonstructural protein
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C;Superfamily: influenza virus nonstructural protein NS1
C;Keywords: alternative splicing; nonstructural protein
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A;Residues: 1-230 <TRE>
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C;Species: influenza A virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
R;Accession: 832662
R;Treanor, J.J. Snyder, M.H.; London, W.T.; Murphy, B.R.
Virology 171, 1-9, 1989
A;Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, A;Reference number: A32662; MUID:8929445; PMID:2525836
                                                                                                                                           C;Accession: C32662
R;Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.
Virology 1171, 1-9, 1989
A;Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, A;Reference number: A32662; MUID:89299445; PMID:2525836
A;Accession: C32662
                                                     nonstructural protein NSI - influenza A virus (strain A/mallard/New York/6750/78)
C;Species: influenza A virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
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92.1%; Score 1079; DB 1; Length 230;
Best Local Similarity 91.7%; Pred. No. 8.2e-86;
Matches 211; Conservative 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 230;
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C,Superfamily: influenza virus nonstructural protein NS1
C,Keywords: alternative splicing; nonstructural protein
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C;Keywords: alternative splicing; nonstructural protein
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93.2%; Score 1092; DB 1;
Best Local Similarity 92.6%; Pred. No. 6.2e-87;
Matches 213; Conservative 9; Mismatches 8;
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A; Residues: 1-230 <TRE>
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A; Residues: 1-230 <TRE>
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nonstructural protein NSI - influenza A virus (strain A/Mynah/Haneda-Thai/76 (H3N1])
C;Species: influenza A virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C;Accession: I27846
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         Virology 158, 465-468, 1987.
Virology 158, 465-468, 1987.
Virology 158, 465-468, 1987.
Virology 158, 465-468, 1987.

Arittle: Genetic divergence of the NS genes of avian influenza viruses.

A.Recession: C27846

A.Molecule type: genomic RNA

A.Mosiques: 1-227 <NAK>

A.Accessives references: GB:M16563; NID:g324786; PIDN:AAA43510.1; PID:g324787
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ViroLogy 158, 465-468, 1987
A;Title: Genetic divergence of the NS genes of avian influenza viruses.
A;Reference number: A94361; MUID:87236215; PMID:2954302
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 90.5%; Score 1061; DB 1; Length 227; Best Local Similarity 91.2%; Pred. No. 2.9e-84; Matches 207; Conservative 11; Mismatches 9; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 GLEWINNTVRVSKTLORFAWRSSNENGRPPLTPKOKRKMARTIRSEV 230
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C;Superfamily: influenza virus nonstructural protein NS1
C;Keywords: alternative splicing; nonstructural protein
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C,Superfamily: influenza virus nonstructural protein NS1
C,Keywords: alternative splicing; nonstructural protein
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Best Local Similarity 90.7%
Matches 206; Conservative
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A, Molecule type: genomic RNA
A, Residues: 1-227 <NAK>
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A; Residues: 1-237 < LAM>
A; Residues: 1-237 < LAM>
A; Residues: 1-237 < LAM>
A; Cross-references: UNIPROT: P03495; GB: V01102; GB: J02169; NID: g60797; PIDN: CAA24288.1; F
A; Experimental source: strain A/Udorn/72 [H3N2]
A; Experimental source: strain A/Udorn/72 [H3N2]
A; Robertson, J.S.
B; Robertson, J.S.
A; Robertson, J.S.
A; Title: S' and 3' terminal nucleotide sequences of the RNA genome segments of influenza A; Reference number: S11286; MUD: 80034428; PMID: 493121
A; Accession: S11297
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C;Species: influenza A virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
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C;Species: influenza A virus
C;Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 09-Jul-2004
C;Accession: A04088; 211297
C;Accession: A04088; C;J.
Ccll 21, 475-485, 1980
A;Tille: Sequence of interrupted and uninterrupted mRNAs and cloned DNA coding for the A;Reference number: A90801; MUID:81001890; PMID:7407920
A;Reference number: A04088
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MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETAIRA
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A;Experimental source: strain A/FPV/Rostock/34 [H7N1]
A;Note: the authors translated the codon CAG for residue 10 as Glu
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C;Superfamily: influenza virus nonstructural protein NS1
C;Keywords: alternative splicing
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Best Local Similarity 90.4%;
Matches 208; Conservative 1
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A; Residues: 1-15 < ROB>
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nonstructural protein NS1 - influenza A virus (strain A/Tern/South Africa/61 [H5N3]) (fr.
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                                                                                                                                                                                                                                                                                                                          C;Species: influenza A virus
C;Daces 30-58p-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C;Accession: E27846
R;Nakajima, K.; Nobusawa, B.; Ogawa, T.; Nakajima, S.
Virology 18, 465-4468, 1987
A;Title: Genetic divergence of the NS genes of avian influenza viruses.
A;Reference number: A94361; MUID:87236215; PMID:2954302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NTVSSFQVDCFLWHVRKRFADQELGDAPFLDRLRRDQKSLRGRGSTLGLDIETATRAGKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: genomic RNA
A;Residues: 1-227 <NAK>
A;Cross-references: GB:M16564; NID:g324875; PIDN:AAA43572.1; PID:g324876
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                                                                                                                             181 LIGGLEWNNNTVRVSKTLORFAWRSSNENGRPPLTPKOKRKMARTIRSEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 89.6%; Score 1050; DB 1; Length 2 Best Local Similarity 91.2%; Pred. No. 2.6e-83; Matches 207; Conservative 9; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: segment 8
C;Superfamily: influenza virus nonstructural protein NS1
C;Keywords: alternative splicing; nonstructural protein
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Job time : 34.1083 secs
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R;Porter, A.G.; Smith, J.C.; Emtage, J.S.
R;Port. Natl. Acad. Sci. US.A. 77, 5074-5078, 1980
A;Title: Acadeoide sequence of influenza virus RNA segment 8 indicates that coding reginal R;Reference number: A93858; MUID:81054909; PMID:6254054
A;Accession: A04091
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C;Accession: A32662
R;Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.
Virology 171, 1-9, 1989
A;Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, A;Reference number: A32662; MUID:89299445; PMID:2525836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nonstructural protein NSI - influenza A virus (strain A/pintail/Alberta/268/78)
C;Species: influenza A virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
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                                                                                                                                             nonstructural protein NS1 - influenza A virus
C;Species: influenza A virus
C;Date: 31-Oct.1980 #sequence_revision 31-Oct-1980 #text_change 30-Sep-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETAIRA
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Length 230;
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89.6%; Pred. No. 9.8e-84;
ive 13; Mismatches 11; Indels
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C;Superfamily: influenza virus nonstructural protein NS1
C;Keywords: alternative splicing
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C;Superfamily: influenza virus nonstructural protein NS1
C;Keywords: alternative splicing; nonstructural protein
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ilarity 88.3%; Pred. No. 6.6e-84;
Conservative 16; Mismatches 11;
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Best Local Similarity 89.6'
Matches 206; Conservative
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A; Residues: 1-230 <TRE>
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203; Conserv
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A; Residues: 1-230 < POR>
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Matches
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1 MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETAIRA
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Non-Beructural protein NS1.
Influenza A virus (A/Albany/6/58 (H2N2)).
Influenzavirus A; H2N2 subtype.
Influenzavirus A; H2N2 subtype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Lindstrom S.E., Cox N.J., Klimov A.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AV210157; AAO46579.1;
HSSP; P03495; 1A1L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR000256; Flu NSI.
InterPro; IPR00968; SIS7NSI_bind.
PFMOM: PF00600; Flu NSI; 1.
Probom; PD006013; Flu NSI; 1.
SEQUENCE 237 AA; 26914 MW; 88C4D124B449EEC3 CRC64;
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96.5%; Pred. No. 1.2e-88;
tive 6; Mismatches 2;
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VNS1 IAUSS

LD VNS1 IAUSS

STANDARD; PRT; 237 AA.

AC P03498;

DT 21-UUL-1986 (Rel. 01, Last sequence update)

DT 21-UUL-2004 (Rel. 44, Last annotation update)

DR Obstructural protein NS1.
                                                                                                                                                                                                                                                                                                                                 237 AA
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                                                                         099403
06XTF6
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0910P3
06XTC6
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OCXTE6
OCXTG4
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Best Local Similarity
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Q61d08 influenza
Q76mt8 influenza
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1 MDPNTVSSFQVDCFLMHVRK.....RPPLTPKQKRKMARTIRSEV 230
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                  1612378 segs, 512079187 residues
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                                                                                                         2005, 21:32:32
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VNS1 IAUSS
QGXTI4
QGXTI6
QGXTG
VNS1 IALE1
QGXTJ2
QGXTJ3
QGXTJ3
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Q71QT3
Q6XTG8
Q9DUT8
VNS1 IALEN
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Maximum Match 100%
Listing first 45 summaries
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Match Length DB
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                                                                                                          September 22,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                      Krystal M., Buonagurio D.A., Young J.F., Palese P.; "Sequential mutations in the NS genes of influenza virus field
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.4%; Score 1142; DB 1; Length 237; Best Local Similarity 97.0%; Pred. No. 1.4e-88; Matches 223; Conservative 4; Mismatches 3; Indels C
                  Influenza A virus (strain A/USSR/90/77 H1N1).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-structural protein NS1.
Influenza A virus (A/SaoPaolo/3/59(H2N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A, H2N2 subtype.
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Lindstrom S.E., Cox N.J., Klimov A.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00600; Flu NS1; 1.
ProDom; PD006613; Flu NS1; 1.
Alternative splicing; NS1; 1.
SEQUENCE 237 AA; 26890 MW; D5759FBBE558E268 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                     IsoId=P03498-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                      lsoId=P03504-1; Sequence=External;
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05-JUL-2004 (TrEMBLrel. 27, Last seq
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InterPro; IPR009068; S157NS1_bind.
                                                                                                                                                                    MEDLINE=83164298; PubMed=6834468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; K00578; AAA43540.1; -. HSSP; P03495; 1NS1.
                                                                                                                                                                                                                                                                   J. Virol. 45:547-554(1983).
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                                                                                            NCBI_TaxID=225083;
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              Name=NS1;
                                                                                                                                                                                                                                                                                                                                                                                               Name=NS2;
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Q6XT14;
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                                                                                                                                                                                                                              Length 237;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Non-structural protein NS1.
Influenza A virus (A/Victoria/15681/59(H2N2)).
Influenza A virus (A/Victoria/15681/59(H2N2)).
Influenza A virus (A/Victoria/15681/59(HZN2)).
Influenzavirus A; H2N2 subtype.
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Lindstrom S.E., Cox N.J., Klimov A.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY210158; AA046581.1; -.
HSSP; P03495; 1AIL.
EMBL; AY210159; AAO46583.1; -.
HSGP; P01495; IAIL.
GO; G0003723; F:NA binding; IEA.
INTEXPO; IPR000256; F!U, NSI.
INTEXPO; IPR0009068; S15/NSI_bind.
Pfan; PF00600; F!U, NSI; 1.
PrODOM; PR006013; Flu, NSI; 1.
SEQUENCE 237 AA; Z6972 MW; PE0004CAASOCEED7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0033723; F:RNA binding; IEA.
InterPro; IPR000256; Flu NSI.
InterPro; IPR009068; S15/NS1_bind.
Prom; PF00600; Flu NSI; 1.
ProDom; P0000613; Flu NSI; 1.
SEQUENCE 237 AA; 26972 MM; FE0004CAA50CEED7 CRC64;
                                                                                                                                                                                                                              97.4%; Score 1142; DB 2; 96.5%; Pred. No. 1.4e-88;
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                                                                                                                                                                                                                                                                                5; Mismatches
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                                                                                                                                                                                                                           Query Match
Best Local Similarity 96.5%;
                                                                                                                                                                                                                                                                                Matches 222; Conservative
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Matches 222; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 QAIMDKNIILKANFSVIFDRLETLILLRAFTEEGAIVGEISPLPSLPGHTNEDVKNAIGV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETAIRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.4%; Score 1141; DB 1; Length 230; 96.5%; Pred. No. 1.7e-88; tive 5; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000256; Flu NS1.
InterPro; IPR009068; S15/NS1_bind.
Pfam; PF00600; Flu NS1; 1.
ProDom; PD000613; Flu NS1; 1.
Alternative splitsing; Nonstructural protein.
SEQUENCE 230 AA; 26096 MW; D3B867B15A70CE97 CRC64;
Event-Alternative splicing; Named isoforms=2;
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                                                           IsoId=P26131-1; Sequence=Displayed;
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EMBL; M81578; AAA19201.1; ALT_TERM.
EMBL; M8184; AAA19203.1; ALT_TERM.
HSSP; P03495; 1NS1.
                                                                                                                       P26133-1
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Matches 222; Conservative
                                                                                                                                                       Sequence=External;
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                                                                                                                    IsoId=P21432-1,
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                               Name=NS1
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QEXTJ2;
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   181 LIGGLEWNDNTVRVSKTLQRFAWRSSNENGRPPLTPKOKRKMARTIRSKV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 LIGGLEWNNTVRVSKTLQRFAWRSSNENGRPPLTPKQKRKMARTIRSEV 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 237;
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Influenza A virus (strain A/Leningrad/134/17/57 H2N2), and
Influenza A virus (strain A/Leningrad/134/47/57 H2N2).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
                                                                                                                                                                                                                                                                                                 Non-structural protein NS1.
Influenza A virus (A/Davis/1/57(H2N2)).
Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A; H2N2 subtype.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEGUENCE FROM N.A.
Lindstrom S.E., Cox N.J., Klimov A.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AY210153; AAO46571.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR000256; Flu_NS1.
InterPro; IRR009068; S15/NS1_bind.
PFam; PF00600; Flu_NS1; 1.
PFDOM; PD000613; Flu_NS1; 1.
SEQUENCE 237 AA; 26972 MW; 88D2935CF44095D6 CRC64;
                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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01-MAY-1992 (Rel. 22, Last sequence update)
02-UUL-2004 (Rel. 44, Last amotation update)
Nonstructural protein NS1.
                                                                                                                                                       237 AA
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MEDLINE=92124758; PubMed=1733114;
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AC P26131;
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Matches
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Length 237;
                                                                                                                         Influenza A virus (A/BlSalvador/2/57(H2N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A; H2N2 subtype.
                                                                                                                                                                                                                                                                                                                        Lindstrom S.E., Cox N.J., Klimov A.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY210155; AA046575.1; -.
HSSP; P03495; IAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR000256; Flu NS1.
InterPro; IPR009668; SIS/NS1_bind.
Pfam; PF00600; PIU NS1; 1.
Probom; PD00613; Flu NS1; 1.
SEQUENCE 237 AA; 26943 MW; 88D293408EE944C3 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Alternative splicing; Nonstructural protein. SEQUENCE 237 AA; 26889 MW; 3B80159BFD79F212 CRC64;
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                                                                                              61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWFMLMPKQKVAGPLCIRMD 120
                                                                                                              GKQIVERILKEESDEALKATMASAPASRYLTDMTIEEMSRDWFWLMPKQKVAGPLCIRMD 120
                                                                                                                                                      QAIMDKSIILKANPSVIFDRLETLILLRAFTEEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
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                                                        1 MDPNTVSSFQVDCFLWHVRKQVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETATRV
                                        1 MDPNIVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETAIRA
                Gaps
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"Variation in nucleotide sequences coding for the N-terminal regions of the matrix and nonstructural proteins of influenza A viruses.";
J. Virol. 38:1-7(1981).
-1. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INOIG=P01505-1; Sequence=External; MISCELLANEOUS: Partial sequence of A/RI/5-/57 is identical with
                                                                                                                                                                                                             LIGGLEWNNNTVRVSKTLORFAWRSSNENGRPPLTPKOKRKMARTIRSEV 230
                                                                                                                                                                                                                          181 LIGGLEWNDNTVRVSKTLQRFAWRSSNEDGRPPLTPKQKRKMARTIRSKV 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=A/Fort Warren/1/50;
MEDLINE=83164298; PubMed=6834468;
Krystal M., Buonagurio D.A., Young J.F., Palese P.;
"Sequential mutations in the NS genes of influenza virus field
                                                                                                                                                                                                                                                                                                                                                                                                        Influenza A virus (strain A/Fort Warren/1/50 H1N1), and Influenza A virus (strain A/R/5-/57 H2N2).
Viruses, sRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
              2; Indels
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 96.5%; Pred. No. 1.7e-88;
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                                                                                                                                                                                                                                                                                                            237 AA
             6; Mismatches
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InterPro; IPR009068; S15/NS1_bind.
Pfam; PF00600; Flu NS1; 1.
ProDom; PD000613; Flu_NS1; 1.
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MEDLINE=81218398; PubMed=7241645;
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HSSP; P03495; 1NS1.
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J. Virol. 45:547-554(1983)
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 Best Local Similarity 96.5
Matches 222; Conservative
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Local Similarity 96.1%; Pred. No. 2.5e-88;
les 221; Conservative 6; Mismatches 3; Indels (
           Length 237;
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Influenza A virus (A/Chile/13/57(H2N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A; H2N2 subtype.
                                                   Indels
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Lindstrom S.E., Cox N.J., Klimov A.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY210154; AA046573.1; -...
HSSP; P03495; IAIL.
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InterPro; IPR000256; Flu NS1.
InterPro; IPR00968; S157NS1_bind.
Pfam; PF00600; Flu NS1; 1.
Probon; PD006613; Flu NS1; 1.
SEQUENCE 237 AA; 27004 MW; 29158F21429BF365 CRC64;
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
97.3%; Score 1140; DB 1;
96.5%; Pred. No. 2.1e-88;
:ive 6; Mismatches 2;
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       Query Match
Best Local Similarity 96.5'
Matches 222; Conservative
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                                                                                                        Influenza A virus (A/Albany/7/57 (H2N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A; H2N2 subtype.
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Influenzavirus A; H2N2 subtype.
NCGI_TaxID=221935;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Linderrom S.B., Cox N.J., Klimov A.;
Submitred (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY210152; AA046569.1;
HSSP; P03495; IAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lindstrom S.E., Cox N.J., Klimov A.;
Submitted (JAN-2003) to the BMBL/GenBank/DDBJ databases.
EMBL; AX210160; AAO46585.1; -.
HSSP; P03495; 1AIL.
                                                                                                                                                                                                                                                                                                                                           GO; GO:0003723; F.RNA binding; IEA.
InterPro; IPR000256; Flu NS1.
InterPro; IPR009668; S15/NS1_bind.
Pfam; PF00600; Flu NS1; 1.
Probom; PD006013; Flu NS1; 1.
SEQUENCE 237 AA; 26944 MW; AA829935CF4533C5C CRC64;
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ProDom; PD000613; Flu NS1; 1.
SEQUENCE 230 AA; 26089 MW; 0A6DE9DEF3019F70 CRC64;
              05-UUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Non-structural protein NS1.
Influenza A virus (A/Philippines/2/60(H2N2)).
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InterPro; IPR000256; Flu NS1.
InterPro; IPR009068; S15/NS1_bind.
                                                                                     Non-structural protein NS1.
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Best Local 9
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Best Local
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Q6XTI2;
Q6XTJ8
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Gaps

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1 MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETAIRA 60

Matches 220; Conservative

Similarity

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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                                                                                                                   61 GKQIVERILKEESNEALKATMASTPASRYLTDMTIEEMSRDWFWLMPKQKVAGPLCIRMD 120
                                                                                                                                                                                             QAIMDKSIILKANFSVIFDRLETLILLRAFTEEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
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9
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                                                                                   GKOIVERILKEESDEALKMTMASAPASRYLTDMTIBEMSRDWFMLMPKOKVAGPLCIRMD
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MEDLINE-89345097; PubMed-2762132;
Schreier E., Roeske H., Michel S.;
"Nucleotide sequence of the NS gene of influenza virus A/Chile/1/83
                                                                                                                                                                                                                                                                                                           181 LIGGLEWNNTVRVSKTLQRFAWRSSNENGRPPLTPKQKRKMARTIRSEV 230
                                                                                                                                                                                                                                                                                                                                        181 LIGGLEMNDNTVRVSKTLQRFAWRSSNENGRPPLTPKQKRKMARTIRSKV 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=8;
Influenza A virus (strain A/Chile/1/83 H1N1).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00600; Flu NS1; 1. —
Probom; PD000613; Flu NS1; 1. —
Alternative splicing; Nonstructural protein.
SEQUENCE 237 AA; 26819 WW; C33A9E3D0386E752 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1989 (Rel. 12, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
02-CCT-2004 (Rel. 45, Last annotation update)
Nonstructural protein NS1.
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IsoId=P11618-1; Sequence=Dïsplayed;
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InterPro; IPR009068; S157NS1_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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P11618;
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VNS1 IACHI
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61 GKQIVERILKEESDBALKATMASAPASRYLTDMTIEEMSRDWFWLMPKQKVAGPLCIRMD 120
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"Evolution of human influenza A viruses over 50 years: rapid, uniform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLNIETAIRA
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                                     asse.";
Thesis (1994), Molecular Genetics and Microbiology, U.M.D.N.J.-Robert
Wood Johnson Medical School.
EMBL; UJ3682; AAA1580.1; -.
HSSP; P03495; 1NS1.
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strain-specific and host cell-dependent variations in progeny virus
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MEDLINE-86208139; PubMed-2939560;
Buonagurio D.A., Nakada S., Parvin J.D., Krystal M., Palese P.,
                                                                                                                                                                                                                                                                                                                                                                                                             95.9%; Score 1124; DB 2; Length 230; 94.8%; Pred. No. 4.6e-87; tive 7; Mismatches 5; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.8%; Score 1123; DB 2; Length 233; 96.9%; Pred. No. 5.6e-87; tive 5; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
NCBI_TaxID=11320;
                                                                                                                                                                                       GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR000256; Flu NS1.
InterPro; IPR009068; S15/NS1_bind.
Prom; PF00600; Flu NS1; 1.
Probon; P0000613; Flu NS1; 1.
SEQUENCE 230 AA; 26040 MW; 03D355F2EA3AC5A8 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Nonerructural protein 1 (Fragment).
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GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR000256; Flu NS1.
InterPro; IPR009068; 315/NS1_bind.
Pfam; PP00600; Flu NS1; 1.
ProDom; PD000613; Flu_NS1; 1.
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Science 232:980-982(1986).
EMBL; M12592; AAA43506.1; --
HSSP; P03495; 1NS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 94.8
Matches 218; Conservative
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Matches 219; Conservative
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Hash P.J., Schlesinger R.W.;
"Replication of neurovirulent and non-neurovirulent human HINI influenza A viruses in mouse brain and nerve cell cultures: virus
                                                                                                                                    181 LIGGLEWNNITVRVSKTLORFAWRSSNENGRPPLIPKOKRKMARTIRSEV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.0%; Score 1125; DB 2; Length 237; 95.2%; Pred. No. 3.9e-87; tive 6; Mismatches 5; Indels (
                                                                                                  LIGGLEWINNTVRVSKTLQRFAWRSSNENGRPPLTPKQKRKMARTIRSEV
                                                                                                                                                                                                                                                                                                                                                          G6XTJ0;

05-JUL-2004 (TrEMBLrel. 27, Created)

05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

Non-structural protein NS1.

Influenca A virus (A/Malaya/16/58(H2N2)).

Viruses; SSRNA negative-strand viruses; Orthomyxoviridae;

Influenzavirus A, H2N2 subtype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
NCBI_TaxID=11320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lindstrom S.E., Cox N.J., Klimov A.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX210156; AA046577.1;
HSSP; P01495; IAIL.
GO: GO:0003723; F:RNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfan, PP00600; Flu NS1; 1.
ProDom; PD000613; Flu NS1; 1.
SEQUENCE 237 AA; 26940 MW; 60BBC406APD784C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                               237 AA
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                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000256; Flu NSI.
InterPro; IPR009068; S157NS1_bind.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 95.2
Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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61 VERILKEESDBALKMTMASAPASRYLTDMTIEEMSRDWFWLMFKQKVAGFLCIRWDQAIM 120	125 DKSIILKANFSVIFDRLETLILLRAFTEEGAIVGEISPLPSLPGHTNEDIKNAIGVLIGG 184	121 DKNIILKANFSVIFDRLETLILLRAFTEEGAIVGEISPLPSLPGHTNEDVKNAIGVLIGG 180
61	125	121

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Search completed: September 22, 2005, 21:46:05 Job time : 145.504 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

September 22, 2005, 21:28:42; Search time 82.3903 Seconds (without alignments) 568.004 Million cell updates/sec Run on:

US-10-654-737-6 Title: Perfect score:

607 1 MDPNTVSSFQDILARISKMQ.....ALQLLLEVEQEIRTFSFQLI 121 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 segs, 386760381 residues

Searched:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Total number of hits satisfying chosen parameters:

2105692

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04: Database

geneseqp20028:* geneseqp2003as:* geneseqp2003bs:* geneseqp20048:* geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* geneseqp1980s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	ion	Influenza		Putative	Bacterial	Human pol		Human	Human the		-	Influenza	Bacterial	Bacterial	Drosophil	_	Chlamydia	Streptoco			Human nov		Phosphati	Human NOV	Human nov	Human pol
	Description	Aae23117	Abb05773	Aab96332	Ads43213	Aam40442	Aam40443	Ads11970	Ads11971	Ads11969	Ads11968	Aae23128	Ads41964	Adn18677	Abb71614	Adn95580	Aay37571	Aaw63043	Adm26084	Aar03991	Ad£74149	Adq66256	Aao22902	Abu65076	Adn61803	Abp69419
SUMMARIES	ID	AAE23117	ABB05773	AAB96332	ADS43213	AAM40442	AAM40443	ADS11970	ADS11971	ADS11969	ADS11968	AAE23128	ADS41964	ADN18677	ABB71614	ADN95580	AAY37571	AAW63043	ADM26084	AAR03991	ADF74149	ADQ66256	AA022902	ABU65076	ADN61803	ABP69419 .
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de	Query Match	97.2	94.7	15.9	15.9	14.2	14.2	14.2	14.2	14.2	14.2	13.8	13.8	13.8	13.7	13.6	13.5	13.5	13.5	13.3	13.3	13.3	13.3	13.3	13.3	13.3
	Score	590	575	96.5	96.5	98	98	98	98	98	98	84	83.5	83.5	83	82.5	82	. 85	82	81	81	81	81	81	81	81
	Result No.	1	71	m	4	S	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	22

Human lip	Human	Novel hum	_	Human pho	_	Protein s	Disease t			Phosphati	Human hea	Caenorhab	Tumour-as	CDIFF-8,	Human PRO	PRO polyp		Novel hum	Antipsori
Abg31896	Aau79749	Adq66093	Abg31895	Aau79750	Abq06887	Abr53314	Adk63498	Adn19029	Adn22707	Aao22903	Adj69356	Aab13326	Abm80698	Aab47149	Adp55147	Adp24771	Adf06826	Adq66447	Adn03898
ABG31896	AAU79749	ADQ66093	ABG31895	AAU79750	ABG06887	ABR53314	ADK63498	ADN19029	ADN22707	AA022903	ADJ69356	AAB13326	ABM80698	AAB47149	ADP55147	ADP24771	ADF06826	ADQ66447	ADN03898
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874	874	881	902	902	163	944	944	944	376	875	952	962	1131	1253	1281	1281	331	777	2000
13.3	13.3	13.3	13.3	13.3	13.3	13.3	13.3	13.3	13.2	13.2	13.2	13.2	13.2	13.2	13.2	13.2	12.8	12.8	12.8
81	81	81	81	81	80.5	80.5	80.5	80.5	80	80	80	80	80	80	80	80	77.5	77.5	77.5
26	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Attenuated influenza vaccine; prophylactic; therapeutic; infection; virucide; mutant; mutein; NS2 protein. ä Katinger Influenza A virus/singapore/1/57/ca NS2 mutant protein. /note= "Encoded by 48-525 bases" (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG Ferko B, Romanova J, Location/Qualifiers AAE23117 standard; protein; 121 AA. 25-SEP-2001; 2001WO-EP011087. 25-SEP-2000; 2000EP-00120896. 21-AUG-2002 (first entry) Katinger H, Egorov A, Misc-difference 8. .9 WPI; 2002-416282/44. Influenza A virus. WO200224876-A2. 28-MAR-2002 Synthetic. AAE23117; AAE23117

Manufacturing live vaccine, by infecting Vero cells with virus, combining cells with serum-free cell culture medium, incubating cells in presence of protease and nuclease, harvesting virus and preparing vaccine. N-PSDB; AAD37061.

Example 4; Page 63; 90pp; English.

The present invention relates to a method for isolating viruses from various sources and for producing live attenuated influenza vaccines in a serum-free African Green monkey kidney (Vero) cell culture under conditions where alterations in the surface antigens of the virus due to adaptive selection are minimised or prevented. The method is useful for the manufacture of whole-virus vaccine, preferably attenuated live vaccine. It is useful for prophylactic or therapeutic administration

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WPI; 2001-126236/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrococcus abyssi
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            Sequence 121 AA;
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                                                                                                                                                                                                                                                                                                                          AAB96332;
                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes an isolated polynucleotide (I) having the complete sequence of the Influenza A/Udorn/72 (H3N2) strain in positive strand, antigenomic message sense. ABA93934 to ABA9394 encode the Influenza A/Udorn/72 (H3N2) strain proteins given in ABB0576 to ABB05774 from the present invention. (I) is useful for designing polymerase chain reaction (PCR) primers for use in a PCR assay to detect the presence of selecting peptides for use in a sample or for designing and selecting peptides for use in an enzyme linked immunosorbant assay to detect the presence of the corresponding protein produced by that segment in a sample, hence is useful in diagnosis and may be modified by mutation to generate new influenza A variant strains. ABA9495 to ABA94039 represent Influenza A/Udorn/72 (H3N2) strain sequencing primers, which are used in an example from the present invention
                                                                                                                                                                                                                   61 RUGKWREQLGQKFEEIRWLIEEVRHKLKITENSFEQITFWQALQLLFEVEGEIRTFSFQL 120
                                                                                                                                                                                                     61 RNGKWREQLGOKFEEIRWLIEEVRHRLKITENSFEQITFWQALQLLLEVEQEIRTFSFQL 120
                                                                                                                                                                 1 MDPNTVSSFQDILMRMSKNQLGSSSEDLNGMITQFESLKLYRDSLGETVMRMGDLHSLQN 60
                                                                                                                                                9
against viral infection, preferably influenza virus infections. The present sequence is Influenza A virus/singapore/1/57/ca (cold adapted) NS2 mutant protein. This sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide encoding complete sequence of influenza A/Udorn/72 and polypeptide, useful in diagnosis and for generating new influenza A variant strains.
                                                                                                                                                1 MDPNTVSSFQDILMRISKMQLGSSSEDLNGIITQFESLKLYRDSLGEAVMRMGDLHSLQN
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Influenza A/Udorn/72 (H3N2) strain; Influenzavirus A; diagnosis;
Influenza A virus; genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Influenza A/Udorn/72 (H3N2) Strain NS2 protein SEQ ID NO:20.
                                                                                            Length 121;
                                                                                          97.2%; Score 590; DB 5; Length 12
95.9%; Pred. No. 7.9e-59;
ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 80; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                        ABB05773 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUN-2001; 2001WO-US019826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUN-2000; 2000US-0213650P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMCY ) AMERICAN CYANAMID CO.
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                           Best Local Similarity .... Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Latham TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-139923/18.
N-PSDB; ABA93943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Influenzavirus A.
                                                                  Sequence 121 AA;
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                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                             RESULT 2
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                                                                                                                                                                                                                                                                                            61 RNGKWREQLGQKFEEIRWLIEEVRHRLKTTENSFEQITFMQALQLFFEVEQEIRTFSFQL 120
                                                                                                                                                                                                                                                         120
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                                                                                                                                                                                                                                                             RNGKWREQLGQKFEEIRWLIEEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSFQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDPNTVSSFQDILMRISKWQLGSSSEDLNGIITQFESLKLYRDSLGEAVMRMGDLHSLQN
                                                                                                                                                                    1 MDSNTVSSFQDILLERMSKMQLGSSSEDLNGMITQFESLKLYRDSLGEAVMRMGDLHLLQN
                                                             Gaps
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Best Local Similarity 27.6*; Pred. No. 0.15;
Matches 29; Conservative 27; Mismatches 42; Indels
DB 5; Length 121;
Query Match 94.7%; Score 575; DB 5; Length 12
Best Local Similarity 94.2%; Pred. No. 4e-57;
Matches 114; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hyperthermophilic archaeon; hyperthermophilic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative P. abyssi ATPase involved in DNA repair #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Forterre P, Thierry JC, Prieur D, Dietrich J,
Querellou J, Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 1003-1006; 1657pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CNRS ) CNRS CENT NAT RECH SCI.
(IFRE-) IFREMER INST FR RECH EXPL MER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB96332 standard; protein; 880 AA.
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ADS43213

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Bacteria.

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                          form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                        20 QLG-SSSEDINGIITQFESLKLYRDSLGEAVMRMGDLHSLQNRNGKWREQLGQKFE---E
                                                                                                                 DB 8; Length 880;
                                                                                                                                                                                                                                                                                                    76 IRWLIBEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSFQL 120
                                                                                                                                                                                                                                                                                                                               Ma Y,
Xue AJ,
                                                                                                               15.9%; Score 96.5; DB 27.6%; Pred. No. 0.15; tive 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 5373; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asundi V, Chen R,
Wehrman T, Xu C,
R, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM40442 standard; protein; 819 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 5373.
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2000US-00488725.
2000US-00552317.
2000US-00598042.
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2000US-00662191.
2000US-00693036.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-DEC-2000; 2000WO-US034263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                  Local Similarity 27.6
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Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-442253/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAIS9598
                                                                      Sequence 880 AA;
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25-APR-2000;
20-JUN-2000;
19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1999;
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19-OCT-2000;
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                                                                                                                 Query Match
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Zhou P,
                                                                                                                                                                  Matches
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    582 ELGPESVBELN---LRIQELEEFHDKYVEAKKSESELRELKNKLEKEKTELDQAFEMLAD 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant DNA construct comprising a promoter positioned to provide
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microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                            cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant DNA construct; transformed plant; improved plant property,
                                                  76 IRWLIBEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSFQL 120
                                                                           Goldman BS
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                                                                                                                                                                                                           ADS43213 standard; protein; 880 AA
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                                                                                                                                                                                                                                                                                                                                                       Bacterial polypeptide #21643.
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HINKLE G J.
SLATER S C.
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(HINK/) (SLAT/) (CHEN/) (GOLD/)

CAOY/)

Cao Y,

Wang D; , Zhao QA;

Ren F, Wa Zhang J,

Qian XB, Yang Y,

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Zhang J, Zhao QA;
          Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic thateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhishin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                19 MOLGSSSEDLNGIITQFESLKLYRDSLGEAVM-RMGDLHSLQNRNGKWREQLGQ----- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                      18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peripheral nervous system, neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                          -KPBEIRWL----IEEVRHRLKITENSFEQITFMQALQLLLEVEQEI 113
                                                                                                                                                                                                                                                                                                           ch 14.2%; Score 86; DB 4; Length 819; 1 Similarity 21.5%; Pred. No. 2.1; 23; Conservative 32; Mismatches 34; Indels
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Yang Y,
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rman T, Xu C, Xue AJ,
Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polypeptide SEQ ID NO 5374.
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2000US-00662191.
2000US-00693036.
2000US-00727344.
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2000US-00552317.
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Wehrman T,
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2000US-00620312.
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Wang Z, Wehr
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-442253/47.
N-PSDB; AAI59599.
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                                                                                                                                              Sequence 819 AA;
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29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukaemia.
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Zhou P,
                                                                                                                                                                                          Local
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and evicetatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous as peripheral nervous injuries, peripheral nervous as peripheral nervous injuries, peripheral nervous as to a lateral neuropathy and localised neuropathies and central nervous system system diseases, such as a lateral sclerosis, and Shy-Drager Syndrome. Other uses include the cutilisation of the activity chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and therapy, drug screening, and thrombolytic activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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g G, z
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Weng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : |:::|| : :|::| |::| |:::| |:::| |:::| |::::| |::::| |::::| |:::::| |::::| |::::| |:::::| |:::::| |:::::| |:::::| |:::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::
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AJ,
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losh M, Xue
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Wang J, Ghosh M,
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Best Local Similarity
Matches 23; Conserv
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be useful in preparing a composition for diagnosing or treating inflammatory, haematopoietic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic contig protein of the invention.
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Best Local Similarity 21.5%; Pred. No. 2.1;
Matches 23; Conservative 32; Mismatches 34; Indels 18; Gaps
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Wang J, Ghosh M, Xue AJ,
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N-PSDB; ADS11371.
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Chen R, Z
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Misc-difference 1
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Wang D,
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                                                                      The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antiinflammatory, neuroprotective, antianaemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoietic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic contig protein of the invention.
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Weng G,
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Wang J, Ghosh M, Xue
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                Example 2; SEQ ID NO 2207; 718pp; English.
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1. .819
/label= Unknown, OTHER
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Chen R, Zhao QA,
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Misc-difference
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Wang D, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72
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Zhou P;

Ma Y;

Wang Z, Ma Y;

CCCX8X41414X8X8X8X8X8X8X8X1114X8X4X114X8XXXXXX

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The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antinflammatory, neuroprotective, antianaemic, cytostatic and vulnerary activities and may

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Page

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23; Conservative
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Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               537 LPIGTASADVAADIAK-----YTSKLMDAIKGTMTEIYNDLSKNTTWKAQLAEDSQGLR 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y;
                                                                                                                                                                                                                                                                                                                                                                                                  19 MQLGSSSEDINGIITQFESLKLYRDSLGEAVM-RMGDLHSLQNRNGKWREQLGQ---- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide, useful in preparing a composition for diagnosing or treating inflammatory, neurodegenerative or stem cell disorders, e.g., aplastic anemia or cancer for promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary; inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell; aplastic anaemia; cancer; wound healing; gene therapy.
                                                                                                                                                                                                                                                                                                     Gaps
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Weng G,
                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 -KFEEIRWL----IEEVRHRLKITENSFEQITFMQALQLLLEVEQEI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : |:::|| : : : | ::| | ::| | ::| | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | :
                                                                                                                                                                                              14.2%; Score 86; DB 8; Length 819; 21.5%; Pred. No. 2.1; ive 32; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang J, Wehrman T, Wang
Wang J, Ghosh M, Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .819
/label= Unknown, OTHER
/note= "OTHER = In-frame STOP codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human therapeutic contig protein - SEQ ID 2205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADS11968 standard; protein; 819 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-SEP-2003; 2003WO-US030720.
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Chen R, Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                  Local Similarity 21.5
     protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-668857/65
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                                                                                                            Sequence 819 AA;
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                                                                                                                                                                                                         Query Match
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RESULT 10 ADS11968

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14.2%; Score 86; DB 8; Length 819;

Sequence 819 AA;

Query Match

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                                                                                                                                                  Manufacturing live vaccine, by infecting Vero cells with virus, combining cells with serum-free cell culture medium, incubating cells in presence of protease and nuclease, harvesting virus and preparing vaccine.
                                                                                                        7
                                                                                                    19 MOLGSSSEDLNGIITQPESLKLYRDSLGEAVM-RMGDLHSLQNRNGKWREQLGQ-----
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Attenuated influenza vaccine; prophylactic; therapeutic; infection; virucide; mutant; mutein; NS2 protein.
                              18;
                                                                                                                                                                                                                                                   72 -KFEEIRWL----IEEVRHRLKITENSFEQITFMQALQLLLEVEQEI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Wild type Tle substituted with Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild type Tle substituted with Thr"
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                                                                                                                                                                                                                                                                                             : |:::|| ::: ||::: ||::: |::: ||::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||::::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||:::: ||::: ||::: ||::: ||:::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::
                                  Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Influenza B virus/vienna/1/99/ca NS2 mutant protein.
                                  34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11. .12
/note= "Encoded by 74-734 bases"
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21.5%; Pred. No. 2.1; tive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE23128 standard; protein; 122 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ferko B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.8%;
25.0%;
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60 NRNGKWREQLGOKFEEIRWLIEEVR------HRLKITENSF--EQITFMQALQL 105
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                                                                                                                 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell eycle pathway modification; plant growth regulator; homologous recombination; plant growth regulator; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                          4 NTVSSFQDILMRISKMQLGSSSED----LNGIITQFESLKLYRDSLGEAVMRMGDLHSLQ
                                                                                           3 NNITITQ-IEWERKKWAIGSSTHSSSVLMKDIQSQFEQLKLRWESYPNLV-KSTDYH---
   Gaps
34;
      44; Indels
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      Mismatches
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      24;
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                                                                                                                                                                                                                                                                                                LLEVEQEIRTFSFOLI 121
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      34; Conservative
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HINKLE G J.
SLATER S C.
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                                                                                                                                                                                                                                                                                                106
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(GOLD/)
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         Matches
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymuclectide encoding a polypeptide from a comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant comprise or soybean. The method of producing a transformed plant cannot an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polymucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for improved plant properties. Improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance, colarance to herbicides, extreme osmotic conditions, pathogens or peste, increased resistance to plant disease, better growth rate by modification

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               homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                            825 SLEBEIEGLVNKINALKANINENERALKSLTEKLEKLKKEEGEIYSRIEEOKKKKEELER 884
cell cycle pathway with plant growth regulators, increased rate of
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                                                                                                                                                                                                                                                                                                          23 SSSEDINGIITQF-----ESLKLYRDSLGEAVMRMGDLHSLQNRNGKWREQLGQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; card tolerance; heat tolerance; pathogen tolerance; pest tolerance; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomanna; bacterial polypeptide.
                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       72 KFEEIRWLIEBVRHR---LKITENSFEQITFMQALQLLLEVEQEIRTFSFQLI
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                                                                                                                                                                                                                                    13.8%; Score 83.5; DB
23.9%; Pred. No. 6.6;
ive 27; Mismatches
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Best Local Similarity 23.99
Matches 27; Conservative
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HINKLE G J.
SLATER S C.
CHEN X.
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                                                                                                                                                                                                   Sequence 1179 AA;
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comparising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transformed plant with the comparison improved property comprises transformed plant with the recombinant DNA construct and growing the transformed plant where the polynuclectide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. CC The recombinant DNA construct is useful for producing plant properties. CC increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved plant growth and development under at least one stress content, improved plant growth and development under at least one stress production, improved lignin production or improved galactomannan production or improved data for this sequence repersents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPFO at sequence.html.
microbial source. The invention also relates to a transformed plant
%$GGGGGGGGGGGGGGGGGGG
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Sequence 1179 AA;

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23 SSSEDLNGIITQF-----ESLKLYRDSLGEAVMRMGDLHSLQNRNGKWREQLGQ 71
                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                              15;
13.8%; Score 83.5; DB 8; Length 1179; 23.9%; Pred. No. 6.6; tive 27; Mismatches 44; Indels 15
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             Query Match
Best Local Similarity
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Drosophila melanogaster polypeptide SEQ ID NO 41634 ABB71614 standard; protein; 996 AA. 26-MAR-2002 ABB71614; RESULT 14 ABB71614

(first entry)

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

Drosophila melanogaster.

WO200171042-A2.

27-SEP-2001.

23-MAR-2000; 2000US-0191637P 11-JUL-2000; 2000US-00614150

23-MAR-2001; 2001WO-US009231

(PEKE) PE CORP NY.

Li PWD, Adams M, Venter JC,

WPI; 2001-656860/75. N-PSDB; ABL15717 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions

Disclosure; SEQ ID NO 41634; 21pp + Sequence Listing; English.

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18
                                                                                                                                                                                                                                                                                                                                                                                 2 DPNTVSSFQDILMRISKMQLGSSSEDLNGIITQFESLKLYRDSLGEAVMRMGDLH----- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic endothelial cells (LEC) comprises contenting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation correlates with lymphoedema in human subjects, and with the proviso that the LEC protein is not VEGFR-3; and administering to the subject a composition comprising a lymphatic growth agent selected from VEGF-C or
                                                                                                                                                                                                                                                                                                                                                                                                                                      57 --SLONRNGKWREQLGQKFEEIRWLIEEVRHRLKITENSFEQITFWQALQLLLEVEQEI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175 and the encoded proteins (ABBS7737-ABB2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      growth; differentiation; blood endothelial cell; BEC; lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3; lymphatic growth agent; VEGFC, VEGF-D; antiangiogenic; cytostatic; vasotropic; antiinflammatory; gene therapy; endothelial cell disorder; inflammatory disease; cancer metastasis; lymphatic system; human.
                                                                                                                                                                                                                                                                                                                   24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Petrova T, Saharinen P, Saharinen J;
                                                                                                                                                                                                                                                                         13.7%; Score 83; DB 4; Length 996; 26.1%; Pred. No. 6;
                                                                                                                                                                                                                                                                                                                   25; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human BEC/LEC-related protein sequence SeqID503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 503; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADN95580 standard; protein; 236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LUDW-) LUDWIG INST CANCER RES. (LICN ) LICENTIA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAR-2002; 2002US-0363019P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-2003; 2003WO-US006900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                     31, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alitalo K, Makinen T,
                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-876899/81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADN95581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003080640-A1.
                                                                                                                                                                                                                                     Sequence 996 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN95580;
                                                                                                                                                                                                                                                                               Query Match
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Matches
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the development of compounds with an antianglogenic, cytostatic, vasorropic or antiinflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary lymphedema, in screening for an endothelial cells, in treating hereditary lymphedema, in screening for an endothelial cells or two disorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the disferential modulation of blood vessel endothelial cell or lymphatic vessel endothelial cell growth or differentiation. The lymphatic growth agent may also be used in manufacturing a medicament of hereditary lymphoedema resulting from a mutation in a the treatment of hereditary lymphoedema resulting from a mutation in a carcine in finammatory diseases involving the lymphatic vessels, such as various inflammatory diseases involving the lymphatic vessels, such as various inflammatory diseases involving the lymphatic vessels, such as various inflammatory diseases into the method of the invention. Note: This sequence does not appear in the specification but was obtained by the indexer using the source data given in table 14 of the specification.
VEGF-D polypeptides and polynucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytostatic,
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Sequence 236 AA;

Query Match 13.6%; Score 82.5; DB 7; Length 236; Best Local Similarity 32.0%; Pred. No. 0.94; Matches 32; Conservative 16; Mismatches 29; Indels 23; Gaps

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61 RNGKWREQLGQKFEEIRWLIE--EVRHRL---KITENSFE 95

Search completed: September 22, 2005, 21:42:25 Job time : 86.3903 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

September 22, 2005, 21:33:28; Search time 16.8917 Seconds (without alignments) 689.226 Million cell updates/sec

US-10-654-737-6 607 · Title: Perfect score:

1 MDPNTVSSPQDILMRISKMQ.....ALQLLLEVEQEIRTFSFQLI 121 Sequence:

Gapop 10.0 , Gapext 0.5

BLOSUM62

Scoring table:

283416 283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
[. pir1:*
]: pir2:*
[. pir3:*
]: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	nonstructural prot	nonstructural prot	nonstructural prot			nonstructural prot			NS2 protein - infl		nonstructural prot	_	nonstructural prot	nonstructural prot	nonstructural prot		nonstructural prot		conserved hypothet	hypothetical prote	probable chromosom	nonstructural prot							
SUMMARIES	. QI	MNIVZA	S33685	MNIV62	MNIV2M	MNIVC2	MNIV2W	E45539	MNIV2K	S09649	MNIVXX	MNI V2	MNI VX4	MNI VX 8	MNI VB4	MNI VB1	MNIVB3	MNIVX2	MNIVX6	MNIV2F	MNIV26	B45575	MNIVB7	MNIVBS	MNI VB6	MNIVB8	F75103	T29340	F71190	MNIVB
	DB	-	~	н	-	+	Н	Н	-	N	٦	-	-	-	Н	-1	н	н	Н	Н	H	~	Н	-	Н	н	~	7	~	-1
	Length	121	121	121	121	121	121	121	121	121	118	121	118	118	121	121	121	118	118	108	121	121	121	121	121	121	880	2541	1179	122
de	Query	. 98.4	98.2	97.9	96.9	6.7	96.5	94.7	94.7	94.6	93.7	93.4	92.9	92.9	92.9	92.8	92.1	91.6	90.4	85.2	80.1	78.7	78.3	77.9	77.1	76.9	15.9	14.5	13.8	13.6
	Score	597	296	594	588	587	586	575	575	574	569	567	564	564	564	563	559	556	549	517	486	478	475	473	468	467	96.5	88	83.5	82.5
	Result No.	1	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT 2
S33685
nonstructural protein NS1 - influenza A virus (strain A/WS/33)
C;Species: influenza A virus
A;Variety: strain A/WS/33
C;Species: influenza A virus
A;Variety: strain A/WS/33
C;Species: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: 333685, 832221
C;Accession: S33685, 832221
C;Accession: S33685, Will: 3257, 1993
A;Title: Complete nucleotide sequence of the non-structural gene of the human influenza A;Reference number: S33685, MUID:93275765; PMID:8502573
A;Reference number: acid sequence not shown; translation not shown
A;Residues: 1-121 <WAR>
A;Residues: 1-121 <WAR>
A;Cross-references: UNIPROT:Q06049; EMBL:Z21498; NID:9296585; PIDN:CAA797707.1; PID:g2965

nonstructural prot 22% surface membra	apolipoprotein A-I paramyosin - fluke	hypothetical prote hypothetical prote	dar-18 protein - C hypothetical prote hypothetical prote hypothetical prote	VSG expression sit outer dyndin arm d interaptin - slime hypothetical prote GTP diphosphokinas
MNIV23 A45553	S29565 A60608	T32009 T47145	T51924 T32574 T46248 E83947	B32433 T08101 T14867 T45583 E82697
- C	9 99	000	0000	00000
122	4 4 3 9 4 4 3 9 4 4 3 9 4 4 3 9 4 4 3 9 4 4 3 9 4 4 3 9 4 4 3 9 4 4 4 4	376 952	962 965 1253 470	401 749 1738 . 2152
13.4	13.3	13.25	1222	13.0 13.0 12.0
81.5 81	80.5	080	80 80 80 79.5	79 79 79 78.5
30	0 0 0 0 0 0	1001	4 W W &	4 4 4 4 4 4 4 6 4 0

ALIGNMENTS

Score 596; DB 2; Pred. No. 3.1e-44; 1; Mismatches 1.

Query Match 98.2%; Best Local Similarity 98.3%; Matches 119; Conservative

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C;Genetics:

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Rischreier, E.; Roeeke, H.; Michel, S.
Nucleic Acids Res. 17, 5381, 1989
A,Title: Nucleotide sequence of the NS gene of influenza virus A/Chile/1/83 (HINI).
A,Reference number: A34215; MUID:89345097; PMID:2762132
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C;Species: 19-May-1994 #sequence_revision 19-May-1994 #text_change 24-Sep-1999
C;Date: 19-May-1991; A04095
C;Accession: (92991; A04095
T;Krystal, M.; Buonagurio, D.; Young, J.F.; Palese, P.
J. Virol. 45, 547-554, 1983
A;Title: Sequential mutations in the NS genes of influenza virus field strains.
A;Reference number: A92991; MUID:83164298; PMID:6834468
                                                                                                                                                                                                                                                                                                                                                                                                                         61 RNGKWREQLGGKFEEIRWLIEEVRHRLKITENSFEQITFWQALQLLFEVEGEIRTFSFQL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RNGKWREQLGQKFBEIRWLIEEVRHRLKITENSFEQITFWQALQLLLEVEQEIRTFSFQL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: influenza A virus
Spaces: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Jul-1999
Accession: B34215; S04837
                                                                                                                                                                                                                                                              1 MDPNTVSSFQDILMRISKMQLGSSSEDLNGIITQFESLKLYRDSLGEAVMRMGDLHSLQN
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                                                                                                                                                                                                      Gaps
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A;Cross-references: EMBL:X15282; NID:g60479; PIDN:CAA33356.1; PID:g60481
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                                                                                                                                     Query Match 96.9%; Score 588; DB 1; Length 121; Best Local Similarity 95.9%; Pred. No. 1.5e-43; Matches 116; Conservative 3; Mismatches 2; Indels
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C;Superfamily: influenza virus nonstructural protein NS2
C;Keywords: alternative splicing; nonstructural protein
C;Genetics:
A;Map position: segment 8
C;Superfamily: influenza virus nonstructural protein NS2
C;Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
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A,Status: translation not shown
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Best Local Similarity 95.9°
Matches 116; Conservative
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C,Species: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C;Accession: H31831
R;Cox, N.J.; Kitzme, F.; Kendal, A.P.; Maassab, H.F.; Naeve, C.
Virology 167, 554-567, 1988
A;Title: Identification of sequence changes in the cold-adapted, live attenuated influental A;Reference number: A31831; MUID:89073759; PMID:2974219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: M23968; GB: J04349; GB: M23969; NID: G324860; PIDN: AAA43552.1; PID: g
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
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C;Species: 19-May-1994 #sequence_revision 19-May-1994 #text_change 16-Jul-1999
C;Dacession: D92991; A04095
R;Krystal, M; Buonagurio, D; Young, J.F.; Palese, P.
A;Virol. 45, 547-554, 1983
A;Title: Sequential mutations in the NS genes of influenza virus field strains.
A;Reference number: A92991; MUID:83164298; PMID:6834468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nonstructural protein NS2 - influenza A virus (strain A/Ann Arbor/6/60 [H2N2])
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A;Cross-references: GB:K00576; NID:g324813; PIDN:AAA43524.1; PID:g324814
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                                                                                                                                           Length 121;
                                                                                                                                                                                                         1, Indels
                                                           A,Introns: 10/3
C,Superfamily: influenza virus nonstructural protein NS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Superfamily: influenza virus nonstructural protein NS2
C.Keywords: alternative splicing; nonstructural protein
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Best Local Similarity 96.7 Matches 117; Conservative

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Query Match

A; Molecule type: genomic RNA A; Residues: 1-121 <COX>

A, Accession: H31831

A; Map position: segment

A,Accession: D92991 A,Molecule type: genomic RNA A,Residues: 1-121 <KRY>

us-10-654-737-6.rpr

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Ribeklemishev, A.B.; Blinov, V.M.; Vassilenko, S.K.; Golovin, S.Y.; Karginov, V.A.; Mama-Bioorg. Khim. 11, 641-645, 1985
A; Title: Synthesis, cloning and sequencing of a full-length DNA copy of the fragment 8 o. A; Reference number: S09648; MUID:85307107; PMID:4038350
A; Accession: S09649
A; Accession: S09649
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A;Cross-references: UNIPROT:P03503; GB:K01332; NID:g324795; PIDN:AAA43514.1; PID:g324796
A;Experimental source: strain A/Alaska/6/77
                                                                                                                                          coding for the
              R;Lamb, R.A.; Lai, C.J.
Cell 21, 475-485, 1980
A;Title: Sequence of interrupted and uninterrupted mRNAs and cloned DNA coding fo A;Reference number: A90801; MUID:81001890; PMID:7407920
A;Reference number: A90801; MUID:81001890; PMID:7407920
A;Residues: 1-121 clANA
A;Cross-references: Call cland and cloned DNA coding fo A;Residues: 1-121 clANA
A;Cross-references: Call cland a;Ross-references: C
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Accession: S09649
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C;Superfamily: influenza virus nonstructural protein NS2
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C;Superfamily: influenza virus nonstructural protein NS2
C;Keywords: alternative splicing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 94.7%;
Best Local Similarity 94.2%;
Matches 114; Conservative
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A; Residues: 1-121 <BEK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Riklimov, A.; Prosch, S.; Schafer, J.; Bucher, D. Arch. Virol. 122, 143-161, 1992
A.Title: Subtype H7 influenza viruses: comparative antigenic and molecular analysis of A;Reference number: A45539; WUID:92109567; PMID:1530908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nonstructural protein NS2 - influenza A virus (strain A/chicken/Brescia/1902 [H7N7])
C;Species: influenza A virus
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 26-May-1994
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C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004
C;Accession: A04094; A90801; Ā04095
R;Buonagurio, D.A.; Kryetal, M.; Palese, P.; DeBorde, D.C.; Maassab, H.F.
A;Virol. 49, 418-425, 1984
A;Title: Analysis of an influenza A virus mutant with a deletion in the NS segment.
A;Reference number: A92994; MUID:84115066; PMID:6363726
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              A;Cross-references: GB:K00577; NID:g324808; PIDN:AAA43521.1; PID:g324809
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                                                                                                                                                                                                               Score 586; DB 1; Length 121;
Pred. No. 2.2e-43;
3; Mismatches 2; Indels
                                                  C;Genetics:
A;Map position: segment 8
C;Superfamily: influenza virus nonstructural protein NS2
C;Keywords: alternative splicing
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C;Superfamily: influenza virus nonstructural protein NS2
C;Keywords: alternative splicing
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Best Local Similarity 95.9%;
Matches 116; Conservative
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A; Molecule type: genomic RNA
A; Residues: 1-121 <BUO>
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A; Residues: 1-121 <KLI>
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nonstructural protein NS2 - influenza A virus (strain A/pintail/Alberta/119/79)
C;Species: influenza A virus
C;Species: influenza A virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 08-Apr-1994
C;Accession: H32662
R;Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.
Virology 171, 1-9, 1989
A;Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, at A;Reference number: A32662; MUID:89299445; PMID:2225836
A;Accession: H32662
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C;Daces: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C;Daces: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C;Daces: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
R;Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.
Virology 188, 465-4468, 1889
Virology 188, 465-4468, 1880
A;Title: Genetic divergence of the NS genes of avian influenza viruses.
A;Reference number: A94361; MUID:87236215; PMID:2954302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NIVSSFQDILMRMSKMQLGSSSEDLNGMITQFESLKLYRNSLGEAVMRMGDLHSLQSRNG
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R;Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.
Virology 158, 465-468, 1987
A;Title: Genetic divergence of the NS genes of avian influenza viruses.
A;Reference number: A94361; MUID:87236215; PMID:2954302
A;Accession: D27846
A;Molecule type: genomic RNA
A;Residues: 1-118 <NAK>
A;Crosstreferences: GB:M16563; NID:g324786; PIDN:AAA43511.1; PID:g324788
C;Genetics:
A;Gene: NS2
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A;Introns: 77
C;Superfamily: influenza virus nonstructural protein NS:
C;Keywords: alternative splicing; nonstructural protein
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92.9%; Score 564; DB 1;
Best Local Similarity 94.9%; Pred. No. 1.7e-41;
Matches 112; Conservative 5; Mismatches 1;
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Pred. No. 1.7e-41;
5; Mismatches 1;
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ilarity 94.9%;
Conservative
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                                     C,Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999 C;Accession: A30086  
R;Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S. Virology 158, 465-468, 1987  
A;Title: Genetic divergence of the NS genes of avian influenza viruses. A;Reference number: A94361; MUID:87236215; PMID:2954302
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C;Species: influenza A virus
C;Date: 30-Apr-1981 #sequence_revision 30-Apr-1981 #text_change 16-Jul-1999
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C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C;Accession: D27846
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C; Superfamily: influenza virus nonstructural protein NS2
C; Keywords: alternative splicing; nonstructural protein
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C,Superfamily: influenza virus nonstructural protein NS2
C,Keywords: alternative splicing
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Pred. No. 9.4e-42;
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Best Local Similarity 93.4%;
Matches 113; Conservative
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A; Residues: 1-118 <NAK>
               Species: influenza A virus
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6

Gaps

Molecule type: genomic RNA Residues: 1-121 <TRE>

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    influenza A virus (strains A/pintail/Alberta/268/78 and A/ma

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Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.
Irology 171, 1-9, 1989
Title: The B allele of the NS gene of avian influenza viruses, but not the A allele,
Reference number: A32662; MUID:89299445; PMID:2525836
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Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 19-Oct-1995
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                                                                                                                    Query Match 92.9%; Score 564; DB 1; Length 121; Best Local Similarity 93.4%; Pred. No. 1.7e-41; Matches 113; Conservative 3; Mismatches 5; Indels
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Pred. No. 2.1e-41;
3; Mismatches 5; Indels
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C;Superfamily: influenza virus nonstructural protein NS2
C;Keywords: alternative splicing; nonstructural protein
A;Map position: segment 8 A;Introns: 107 A; Introns: 107 C;Superfamily: influenza virus nonstructural protein NS2 C;Keywords: alternative splicing; nonstructural protein
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1;Residues: 1-121 <TRE>
1;Esperimental source: strain A/pintail/Alberta/268/78
1;Accession: D32662
;Molecule type: genomic RNA
;Residues: 1-121 <TR2>
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Best Local Similarity 93.4*;
Matches 113; Conservative
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STRAIN=A/WS/33; TISSUE=Embryonated;
Husak P.J.;
Husis (1994), Molecular Genetics and Microbiology, U.M.D.N.J.-Robert
Wood Johnson Medical School.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thesis (1994), Molecular Genetics and Microbiology, U.M.D.N.J.-Robert Wood Johnson Medical School.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRESUB=Mouse;
Husak P.J., Schlesinger R.W.;
Husak P.J., Schlesinger R.W.;
Hepilcation of neurovirulent and non-neurovirulent human HINI influenza A viruses in mouse brain and nerve cell cultures: virus strain-specific and host cell-dependent variations in progeny virus
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06xtg3
06xtg5
06xtg9
06xth1
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Influenzavirus A.
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Pred. No. 5.7e-44;
1; Mismatches 0; Indels
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Last annotation update)
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Q6XTJ9
VNS2 IAPIO
Q6XTG7
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Q6XTH1
Q6XTH7
Q6XTH9
Q6XT11
Q77AL4
Q8QLS0
Q41648
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99.2%;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-structural protein 2.
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Best Local Similarity 99.2
Matches 120; Conservative
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 Influenza A virus.
NCBI_TaxID=11320;
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Q6dqj2
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Q6xtf7
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                             1612378 segs, 512079187 residues
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VNS2 IAUSS
006049
VNS2 IAANN
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Q6XTU5
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 2000000000
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Maximum DB
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Gaps

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RNGKWREQLGQKPEEIRWLIEEVRHRLKITENSFEQITFWQALQLLLEVEQEIRTFSFQL 120
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Influenzavirus A.
NCBI_TaxID=11320;
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98.3%; Pred. No. 2.8e-43;
ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                   Interpro; IPR000968; Flu NS2.
Pfam; PF00601; Flu NS2; I.
Alternative splicing; Nonstructural protein.
SEQUENCE 121 AA; 14379 MW; DB9C108190B51584 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR000968, Flu NS2.
Pfam; PF00601; Flu NS2; I.
SEQUENCE 121 AA; 14399 WW; B15C16C794F75B22 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                      98.4%; Score 597; DB 1;
97.5%; Pred. No. 2.3e-43;
iive 2; Mismatches 1
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                                                                                                                  EMBL; K00578; AAA43539.1; -
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Best Local Similarity 97.5
Matches 118; Conservative
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Influenza A virus.
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Best Local Similarity 98.3
Matches 119, Conservative
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                                                                                                                                                                                                                                                                                                   MEDLINE=96082767; PubMed=7483294;
Ward A.C., Azad A.A., McKimm-Breschkin J.L.;
"Changes in the NS gene of neurovirulent strains of influenza affect
splicing.";
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SEQUENCE FROM N.A.
MEDLINE-83164298; Pubmed=6834468;
Krystal M., Buonagurio D.A., Young J.F., Palese P.;
Krystal M., Buonagurio D.A., Young J.F., Palese P.;
"Sequential mutations in the NS genes of influenza virus field
"Sequential mutations in the NS genes of influenza virus field
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 600; DB 2; Length 121;
Pred. No. 1.3e-43;
2; Mismatches 0; Indels
                                                                                                                                                                                     Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
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EMBL, 125720; AAA91329.1; -.

EMBL, 1DD3; X-ray; A/B=59-116.

GO; GO:0019012; C:virion; IEA.

InterPro; IPR000968; Flu_NS2.

Pfam; PP00601; Flu_NS2; I.

NONStructural protein.

EQUENCE 121 AA, 14326 MW; B15C197E22F8E294 CRC64;
                                                                          Last sequence update)
Last annotation update)
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Last annotation update)
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         121 AA
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                                                    Created)
       PRT;
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                                                                       01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Create 21-JUL-1986 (Rel. 01, Last 605-JUL-2004 (Rel. 44, Last Monstructural protein NS2. Name=NS; Synonyms=8;
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Best Local Similarity 98.3³
Matches 119; Conservative
         PRELIMINARY;
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                                                  01-NOV-1996 (TrEMBLrel.
                                                                                                                       Nonstructural protein
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NCBI_TaxID=225083;
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                                                                                                                                                                influenza A virus.
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21-JUL-1986
21-JUL-1986
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SEQUENCE FROM N.A.
MEDLINES-922756; PubMed-8502573;
MEDLINES-922756; PubMed-8502573;
WALC A.C., Azad A.A., Macreadie I.G., Mckimm-Breschkin J.L.;
"Complete nucleotide sequence of the non-structural gene of the human influenca virus strain A/WS/33.";
Nucleic Acids Res. 21:2257-2257(1993).
EMBL; Z21498; CAA79707.1;
                                                                                                                                                                                                                                                                                                                                                                                  1 MDPNTVSSFQDILMEMSKMQLGSSSEDLNGIITQFESLKLYRDSLGEAVWRWGDLHSLQN
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VNS2_IAANN
ID VNS2_IAANN
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Gaps

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120

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61 RNGKWREQLGQKPEEIRWLIEEVRHKLKITENSFEQITFMQALQLLFEVEGEIRTFSFQL 120
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                                    Non-structural protein NS2.
Influenza A virus (A/Malaya/16/58(HZN2)).
Viruses, seRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A, HZN2 subtype.
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Influenza A virus (A/Davis/1/57(H2N2)).
Viruses; SRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A; H2N2 subtype.
NCBI_TaxID=220951;
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SEQUENCE FROM N.A.
Lindstrom S.E., Cox N.J., Klimov A.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY210153; AA046572.1; -.
InterPro; IPR000968; Plu NS2.
                                                                                                                                                                         SEQUENCE FROM N.A.
Lindetrom S.E., COX N.J., Klimov A.;
Lindetrom S.E., COX N.J., Klimov A.;
Submitted (JAN-2003) to the EMBL/Genbank/DDBJ databases.
EMBL, AY210156, AAO46578.1;
-InterPro. IPR000968, Flu. Na2.
Pfam; PF00601; Flu. Na2.;
SEQUENCE 121 AA, 14351 MW; DB9C1097D2D12584 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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96.7%; Pred. No. 4.1e-43;
iive 3; Mismatches 1;
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Best Local Similarity 96.7°
Matches 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence changes in the live attenuated, cold-adapted variants influenza A/Leningrad/134/57 (H2N2) virus."; Virology 186:795-797(1992).
                                                                                                                                                                                                                                                                                   STRAIN=A/Ann Arbor/6/60;
MEDLINE=89073759; PubMed=2974219;
COX N.J. Kitame F., Kendal A.P., Maassab H.F., Naeve C.;
"Identification of sequence changes in the cold-adapted, live attenuated influenza vaccine strain, A/Ann Arbor/6/60 (H2N2).";
Virology 167:554-567(1988).
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                                                                                                                              Influenza A virus (strain A/Ann Arbor/6/60), and
Influenza A virus (strain A/Leningrad/134/57 H2N2).
Viruses, ssRNA negative-strand viruses; Orthomyxoviridae;
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Pfam, PF00601; Flu NS2; T.
Alternative splicing; Notructural protein.
SRQUBNCE 121 AA; 14351 MW; DB9C1097D2D12584 CRC64;
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Last annotation update)
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STRAIN-A/Leningrad/134/57;
MEDLINE-92124758; PubMed=1733114;
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                      01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last seq
05-JUL-2004 (Rel. 44, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M23968; AAA43552.1; -. EMBL; M81572; AAA19198.1; -.
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NCBI_TaxID=135322, 128148;
                                                                                       Nonstructural protein NS2
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                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
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RESULT 8 VNS2_IALE2

OGXTJ1; 05-JUL-2004 (TrEMBLrel. 27, Created)

RESULT 6 Q6XTJ1

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Gaps

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(Rel. 22, Created) (Rel. 22, Last seq

STANDARD;

WNS2 IALE2

25-OCT-2004 (Rel. 45, Last Nonstructural protein NS2.

NCBI_TaxID=152281, 152282;

Influenzavirus A.

SEQUENCE FROM N.A.

Name=NS1; Name=NS2;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDPNTVSSFQDILMRISKMQLGSSSEDLNGIITQFESLKLYRDSLGEAVMRMGDLHSLQN
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                                                     ., Mandler J., Scholtissek C.;
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY210157; AAO46580.1; -.
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Pfam; PP00601; Flu NS2; I.
SEQUENCE 121 AA; 14350 MW; DB9C1D2C64DC9E32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           Nonstructural protein.
SEQUENCE 121 AA; 14349 MW; P472E29D7D471C6F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 590; DB 2;
Pred. No. 9e-43;
3; Mismatches
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95.9%; Pred. No. 9e-43;
:ive 4; Mismatches
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                    MEDLINE=91272515; PubMed=2053297;
Schultz U., Fitch W.M., Ludwig S., Mandle
"Evolution of pig influenza viruses.";
Virology 183:61-73(1991).
EMBL; M5S484; AAA43498.1; -.
GO; GO:0019012; C:virion; IEA.
GO; GO:003723; F:RNA binding; IEA.
InterPro; IPR000256; Flu NS2.
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Influenza A virus (A/Albany/6/58(H2N2))
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                                                                                                                                                                                                                                                                                                           Pfam; PF00600; Flu NS1; 1.
Pfam; PF00601; Flu NS2; 1.
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Matches 117; Conservative
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QEXTK1
ID QEXTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence changes in the live attenuated, cold-adapted variants of influenza A/Leningrad/134/57 (HZN2) virus."; Virology 186:795-797(1992).
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Klimov A.I., Cox N.J., Yotov W.V., Rocha E., Alexandrova G.I.,
Kendal A.P.;
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                                                                                                                                                                                                                    Influenza A virus (strain A/Leningrad/134/17/57 H2N2), and Influenza A virus (strain A/Leningrad/134/47/57 H2N2). Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
NCBI_TaxID=11320;
[1]
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InterPro; IPR000968; Flu NS2.
Pfam, PF00601; Flu_NS2.
Alternaries splicing; Nonstructural protein.
SEQUENCE 121 AA; 14333 MW; DB9C1097D2D64844 CRC64;
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Last annotation update)
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                                                                                          Last sequence update)
Last annotation update)
121 AA.
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EMBL; M81578; AAA19200.1; -.

Best Local Similarity 95.9 Matches 116; Conservative

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Query Match

OEXTK1

01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2003 (TrEMBLrel. 25, Nonstructural protein 2.

Influenza A virus.

Name=NS2

PRELIMINARY;

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61 RNGKWREQLGQKPEEIRWLIEEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSFQL 120
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RNGKWREQLGOKFEEIRWLIEBVRHRLKITENSFEOITFMQALQLLLEVEQEIRTFSFQL
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05-JUL.2004 (TrEMBLrel. 27, Last sequence update)
05-JUL.2004 (TrEMBLrel. 27, Last annotation update)
Non-structural protein NS.
Influenza A virus (A/Victoria/15681/59(H2N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A; H2N2 subtype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-structural protein NS2.
Influenza A virus (A/SaoPaolo/3/59(H2N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A; H2N2 subtype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.0%; Score 589; DB 2; Length 12
95.9%; Pred. No. 1.1e-42;
tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Lindetrom S.B., Cox N.J., Klimov A.;
Lindetrom S.B., Cox N.J., Klimov A.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AX210155; AAQ46584.1;
InterPro; IPR000968; Plu NS2.
Pfam; PF00601; Flu NS2; Ī.
SEQUENCE 121 AA; 14339 MW; CB721E67D2D12584 CRC64;
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Lindetrom S.E., COX N.J., Klimov A.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY210158; AAO46582.1; -.
InterPro; IPR000968; Plu NS2.
Pfam; PF00601; Plu NS2; I.
SEQUENCE 121 AA, 14339 WW; CB721E67D2D12584 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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95.9%; Pred. No. 1.1e-42;
iive 3; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                Created)
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Matches 116; Conservative
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KRINE-21904432; PubMed=11907321;

MRDLINE-219044432; PubMed=11907321;

MATOZIN S., Gregory V., Cameron K., Bennett M., Valette M., Aymard M.,

MATOGIN S., Barigazzi G., Lin Y., Bennett M., Valette M., Aymard M.,

Roni B., Barigazzi G., Lin Y., Bay A.;

"Antigenic and genetic diversity among swine influenza A HINI and HINZ

"Yuses in Europe.";

"J. Gen. Virol. 83:735-745(2002).

REMBL; AJ34025; CAC86628.1;

"O GO:0003723; FINA binding; IEA.

REMEL; AJ34025; PLU NS1.

REMEL; PRO00569; FLU NS1.

REMEN; PPO0660; FLU NS2.

REMEN; PPO0660; FLU NS2.

REMEN; PRO0060; FLU NS2.

REMEN; PRO0050; FLU NS2.

REMEN; PRO0050; FLU NS2.

REMEN; PRO0050; FLU NS2.

REMEN; PRO0050; FLU NS2.

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REMEN; PRO0050; FLU NS2.

REMEN; PRO0050; FLU NS3.

REMEN; PRO0050; FLU NS3.

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REMEN; PRO0050; FLU NS3.

REMEN; PRO0050; FLU NS3.

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REMEN; PRO0050; FLU NS3.

REMEN; PRO0050; FLU NS3.

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                                                                                                                                         Influenza A virus (etrain A/Singapore/1/57 H2N2).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A; H2N2 subtype.
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Influenzavirus A; H3N2 subtype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
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                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.
Lindetrom S.B., Cox N.J., Klimov A.;
Lindetrom S.B., Cox N.J., Klimov A.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY210151; AAO46568.1; -.
InterPro; IPR000968; Plu NS2.
Pfam; PP00601; Flu NS2; I.
SEQUENCE 121 AA; 14381 MW; DB8C0196C2C02484 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=NS2;
Influenza A virus (A/Swine/Cote d'Armor/3633/84(H3N2))
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01-UUN-2002 (TrEMBLrel. 21, Created)
01-UNN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Non structural protein 2.
                        05-JUL-2004 (TrEMBLrel. 27, Created)
5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Non-structural protein NS2.
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Best Local Similarity 95.9°
Matches 116; Conservative
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Matches 117; Conservative
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                                                                               61 RNGKWREQLGOKFEEIRWLIEEVRHRLKITENSFEQITFMOALQLLLEVEQEIRTFSFQL 120
                                                                                                        61 RNGKWREQLGQKFEEIRWLIEEVRHKLKTTENSFEQITFMQALQLLFEVEGEIRTFSFQL 120
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1 MDPNTVSSFQDILMRMSKMQLGSSSEDLNGMITQFESLKLYRDSLGEAVMRMGDLHSLQN 60
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MEDILINE=81164-298; bubMed=6814468;
Krystal M., Buonagurio D.A., Young J.F., Palese P.;
"Sequential mutations in the NS genes of influenza virus field
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 96.9%; Score 588; DB 1; Length 121; Best Local Similarity 95.9%; Pred. No. 1.3e-42; Matches 116; Conservative 3; Mismatches 2; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Influenza A virus (strain A/Fort Monmouth/1/47 H1N1).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
NCBI_TaxID=229411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; K00576; AAA43524.1; -.
InterPro; IPR00966; Flu NS2.
Pfam: PF00601; Flu_NS2.
Alternative splicing; Nonstructural protein.
SEQUENCE 121 AA; 14300 MW; ED67C64D21C9BE9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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-!- ALTERNATIVE PRODUCTS:
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Search completed: September 22, 2005, 21:46:06 Job time : 76.4957 secs